

Fig. 1.0

433270 04020350

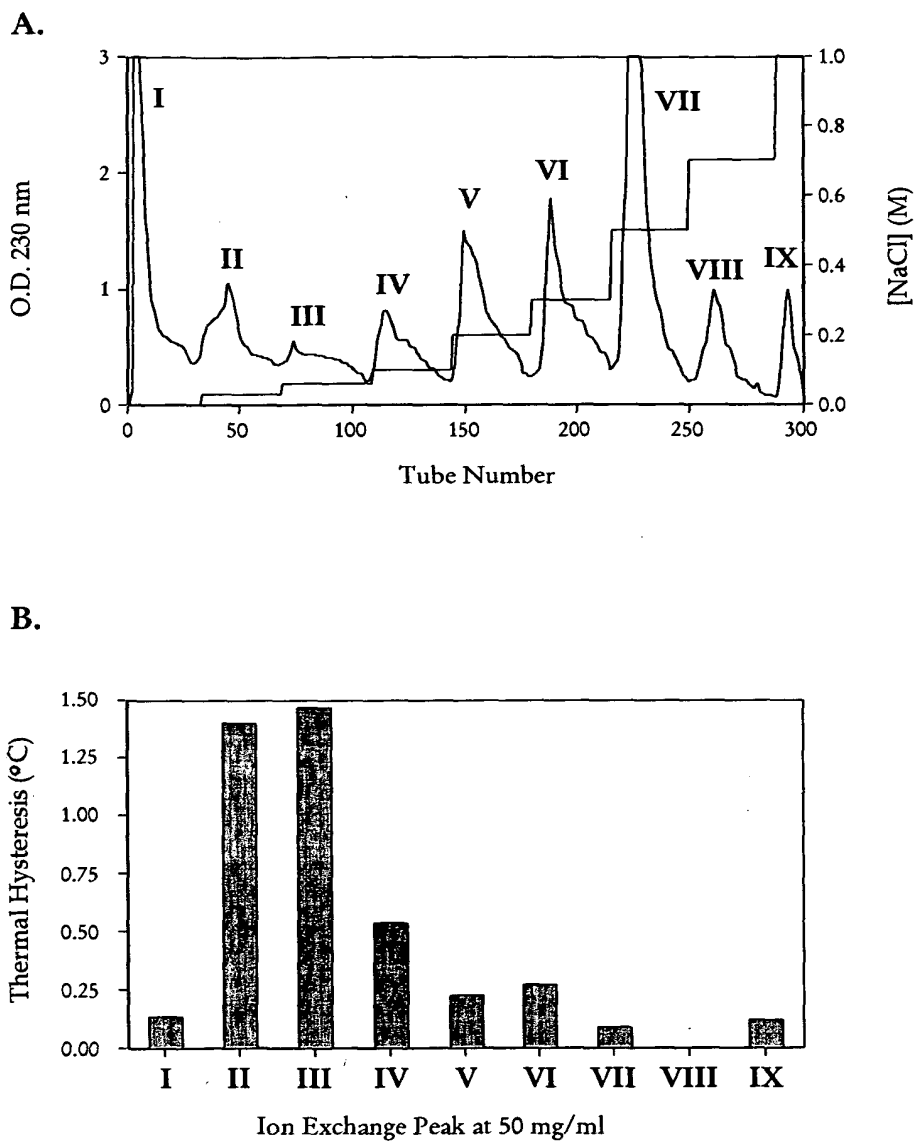


Fig. 1.1

20240419 09:23:00

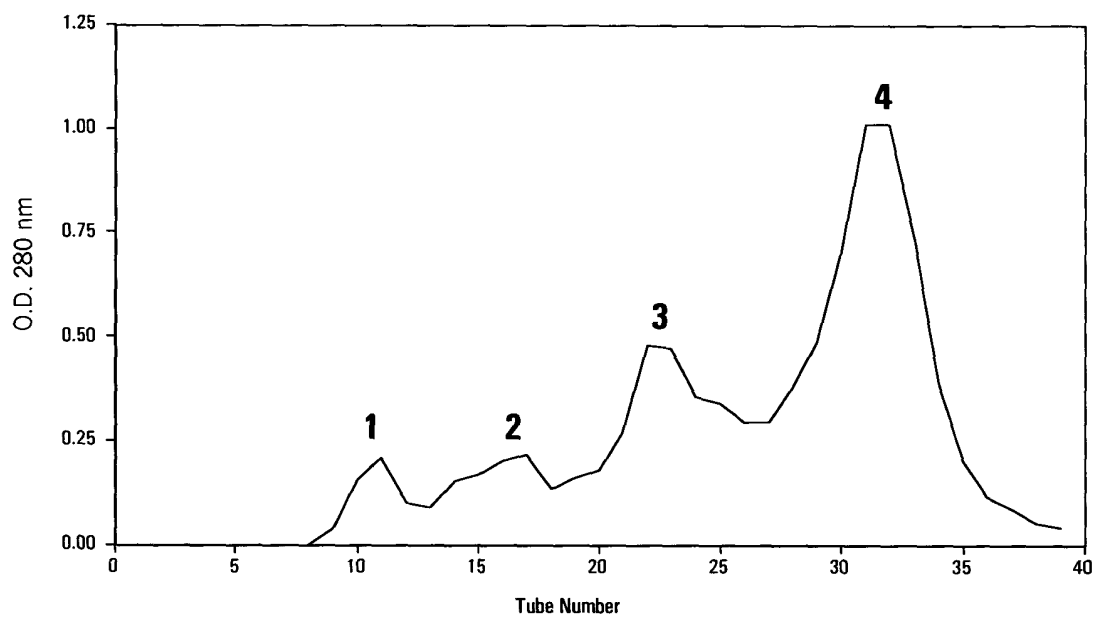


Fig. 1.2

09076349, 012303

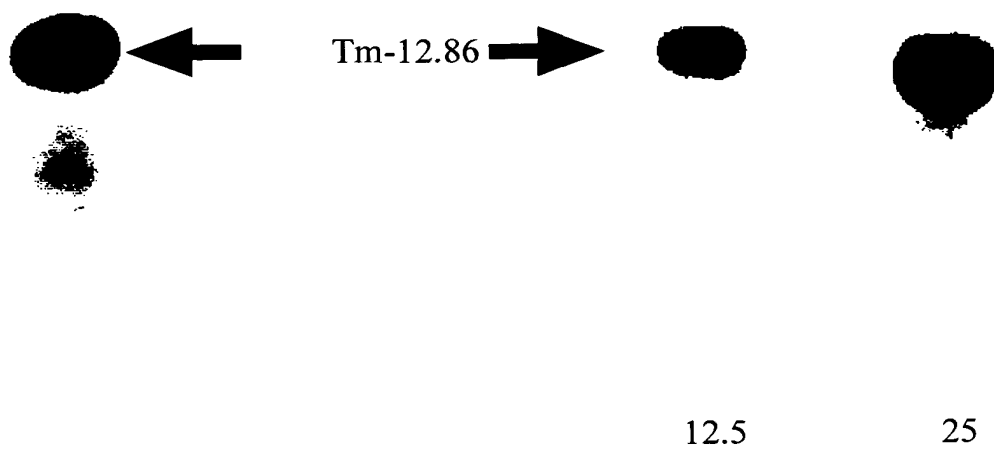


Fig. 1.3

Fig. 1.4

0907540 01294860

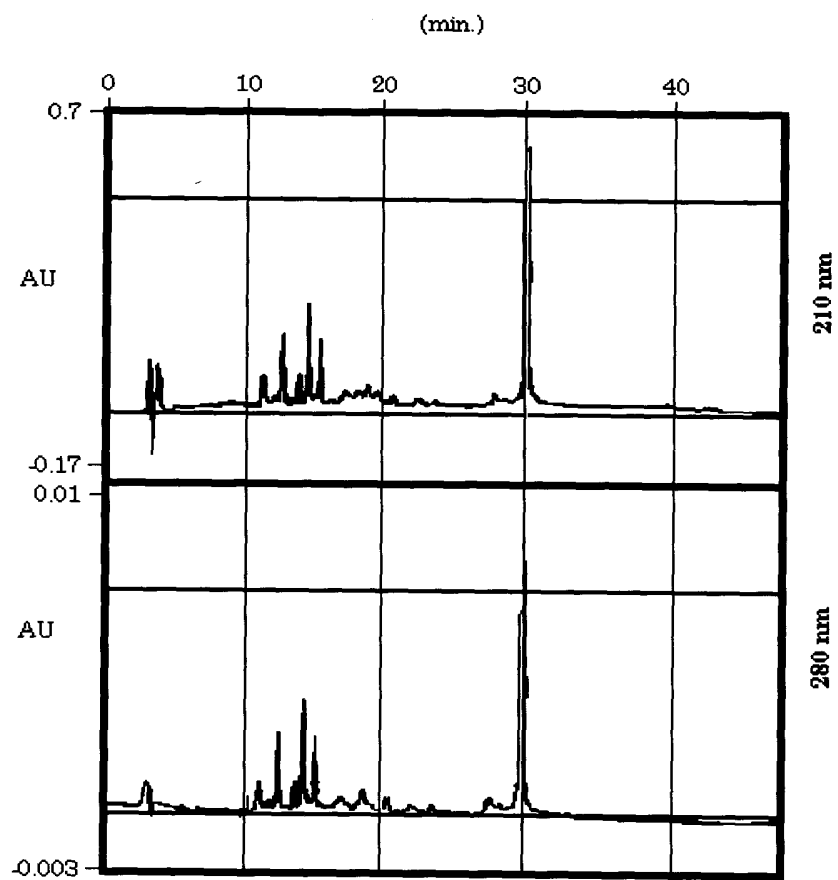


Fig. 1.5

2025-01-23-2025

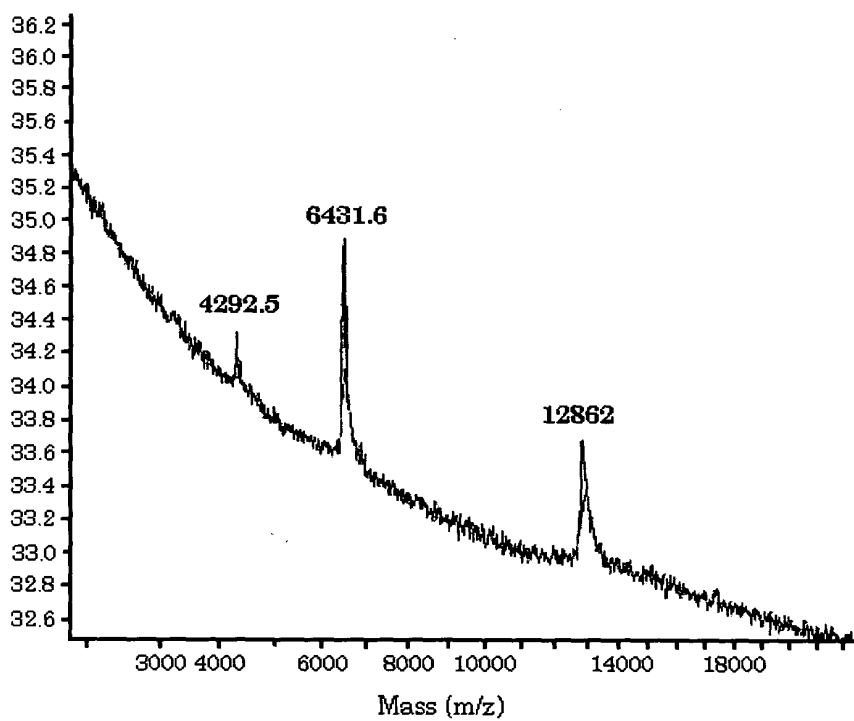


Fig. 1.6

SDS-PAGE gel image showing protein bands. Molecular weight markers (kDa) are indicated on the left: 16.9, 14.4, 10.7, 8.2, 6.2, and 2.5. The gel has two lanes labeled 'w' and 'w/o' at the bottom. An arrow points to a band at 12.86 kDa labeled 'Tm-12.86'.

Fig. 1.7

1. 1. The first
 2. 2. The second
 3. 3. The third
 4. 4. The fourth
 5. 5. The fifth
 6. 6. The sixth
 7. 7. The seventh
 8. 8. The eighth
 9. 9. The ninth
 10. 10. The tenth
 11. 11. The eleventh
 12. 12. The twelfth
 13. 13. The thirteenth
 14. 14. The fourteenth
 15. 15. The fifteenth
 16. 16. The sixteenth
 17. 17. The seventeenth
 18. 18. The eighteenth
 19. 19. The nineteenth
 20. 20. The twentieth
 21. 21. The twenty-first
 22. 22. The twenty-second
 23. 23. The twenty-third
 24. 24. The twenty-fourth
 25. 25. The twenty-fifth
 26. 26. The twenty-sixth
 27. 27. The twenty-seventh
 28. 28. The twenty-eighth
 29. 29. The twenty-ninth
 30. 30. The thirtieth
 31. 31. The thirty-first
 32. 32. The thirty-second
 33. 33. The thirty-third
 34. 34. The thirty-fourth
 35. 35. The thirty-fifth
 36. 36. The thirty-sixth
 37. 37. The thirty-seventh
 38. 38. The thirty-eighth
 39. 39. The thirty-ninth
 40. 40. The fortieth
 41. 41. The forty-first
 42. 42. The forty-second
 43. 43. The forty-third
 44. 44. The forty-fourth
 45. 45. The forty-fifth
 46. 46. The forty-sixth
 47. 47. The forty-seventh
 48. 48. The forty-eighth
 49. 49. The forty-ninth
 50. 50. The fiftieth
 51. 51. The fifty-first
 52. 52. The fifty-second
 53. 53. The fifty-third
 54. 54. The fifty-fourth
 55. 55. The fifty-fifth
 56. 56. The fifty-sixth
 57. 57. The fifty-seventh
 58. 58. The fifty-eighth
 59. 59. The fifty-ninth
 60. 60. The sixtieth
 61. 61. The sixty-first
 62. 62. The sixty-second
 63. 63. The sixty-third
 64. 64. The sixty-fourth
 65. 65. The sixty-fifth
 66. 66. The sixty-sixth
 67. 67. The sixty-seventh
 68. 68. The sixty-eighth
 69. 69. The sixty-ninth
 70. 70. The seventieth
 71. 71. The seventy-first
 72. 72. The seventy-second
 73. 73. The seventy-third
 74. 74. The seventy-fourth
 75. 75. The seventy-fifth
 76. 76. The seventy-sixth
 77. 77. The seventy-seventh
 78. 78. The seventy-eighth
 79. 79. The seventy-ninth
 80. 80. The eightieth
 81. 81. The eighty-first
 82. 82. The eighty-second
 83. 83. The eighty-third
 84. 84. The eighty-fourth
 85. 85. The eighty-fifth
 86. 86. The eighty-sixth
 87. 87. The eighty-seventh
 88. 88. The eighty-eighth
 89. 89. The eighty-ninth
 90. 90. The ninetieth
 91. 91. The ninety-first
 92. 92. The ninety-second
 93. 93. The ninety-third
 94. 94. The ninety-fourth
 95. 95. The ninety-fifth
 96. 96. The ninety-sixth
 97. 97. The ninety-seventh
 98. 98. The ninety-eighth
 99. 99. The ninety-ninth
 100. 100. The hundredth

Fig. 1.8

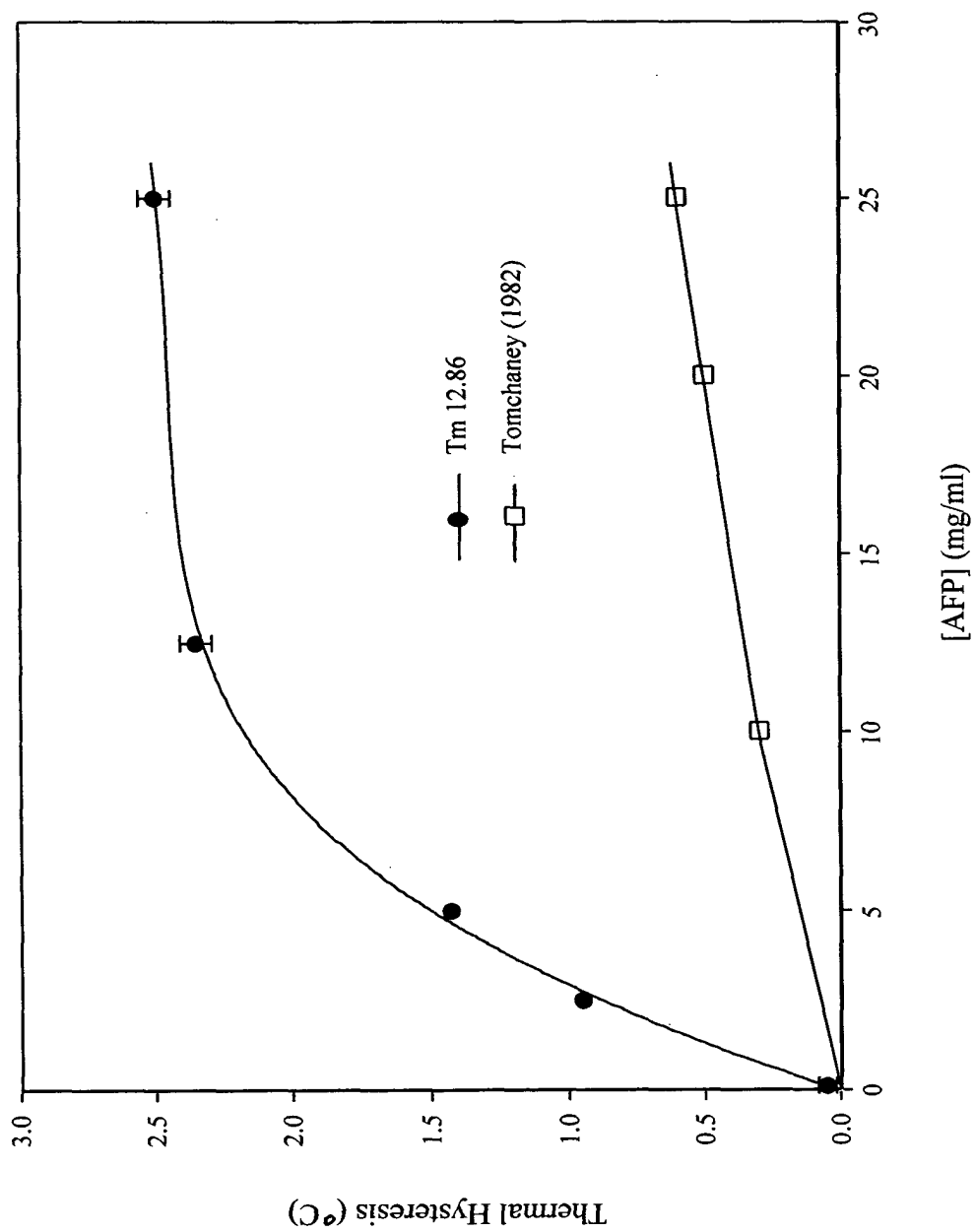


Fig. 1.9

200210 015200

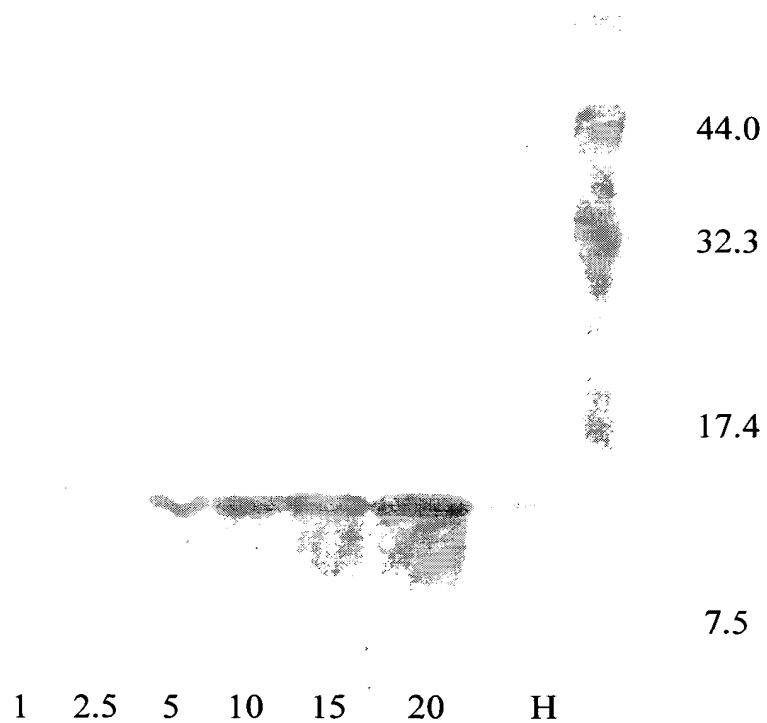


Fig. 1.10

202210 08:22:30

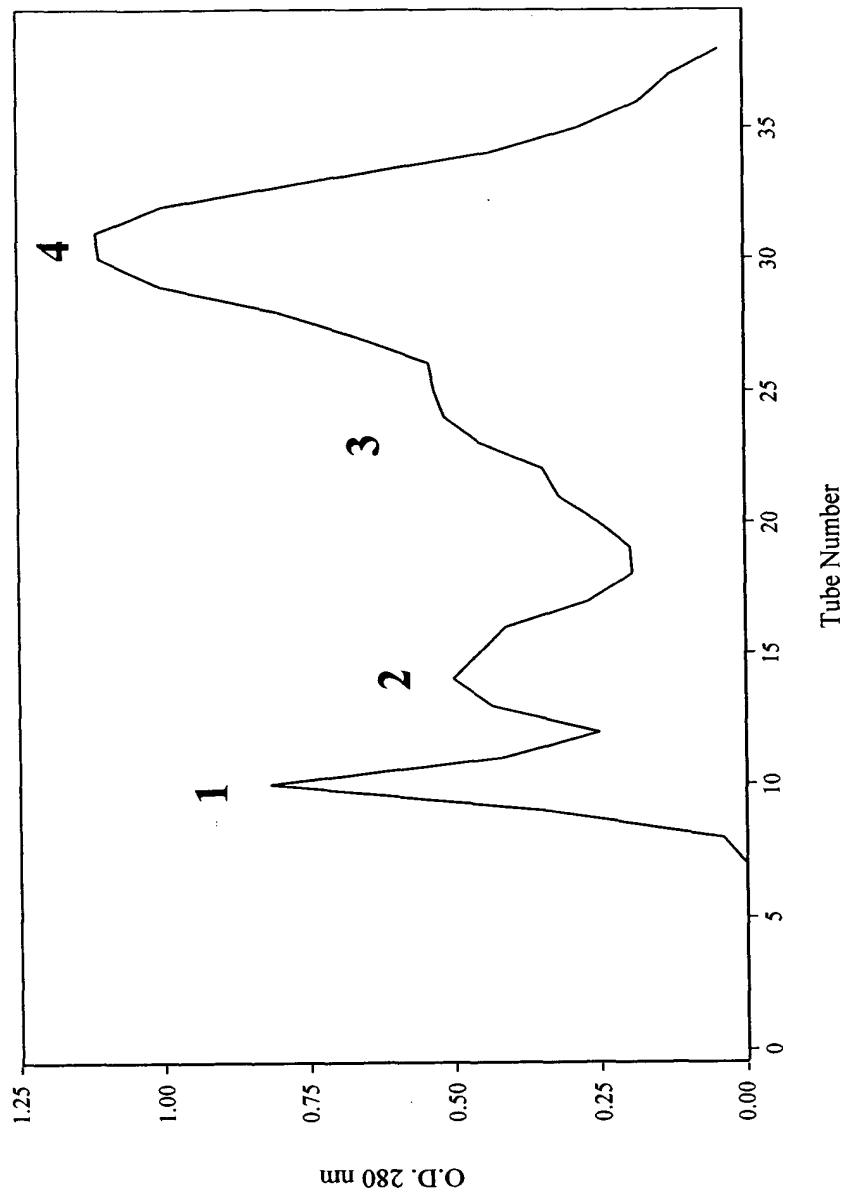


Fig. 1.11

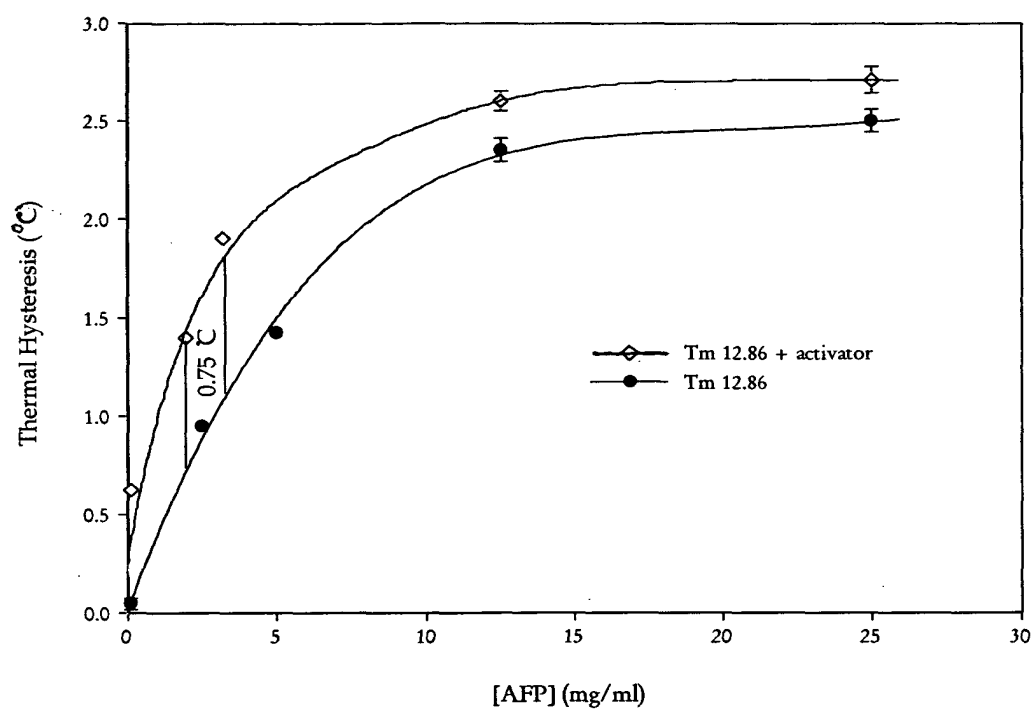


Fig. 1.12

20021010 01:52:00

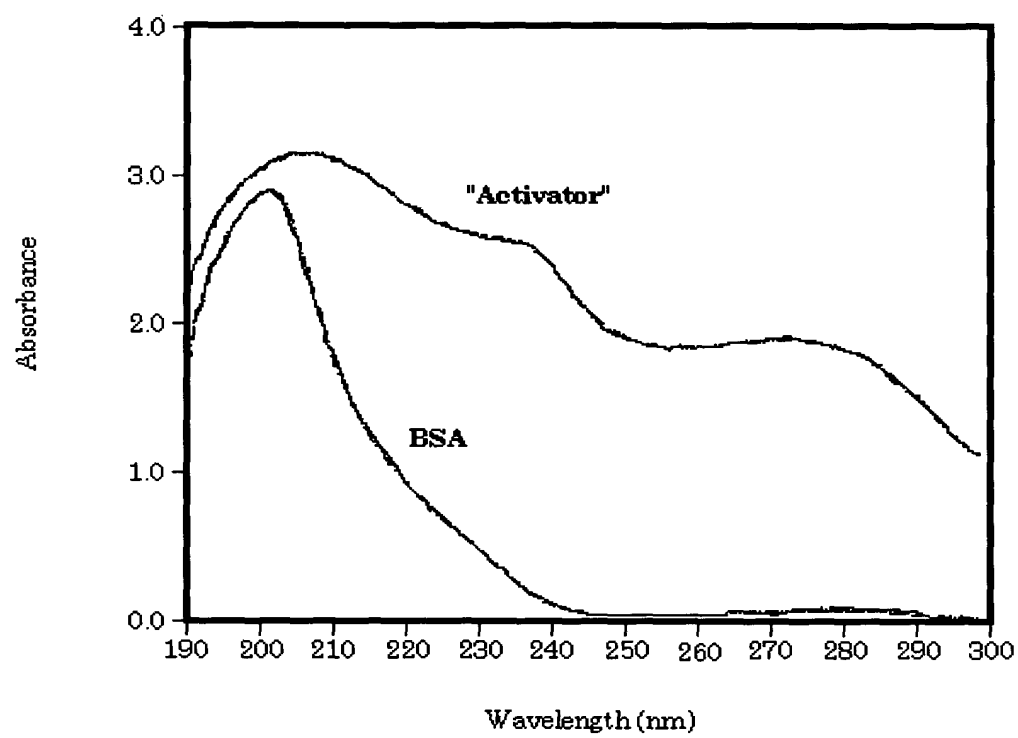


Fig. 1.13

0907348 01203

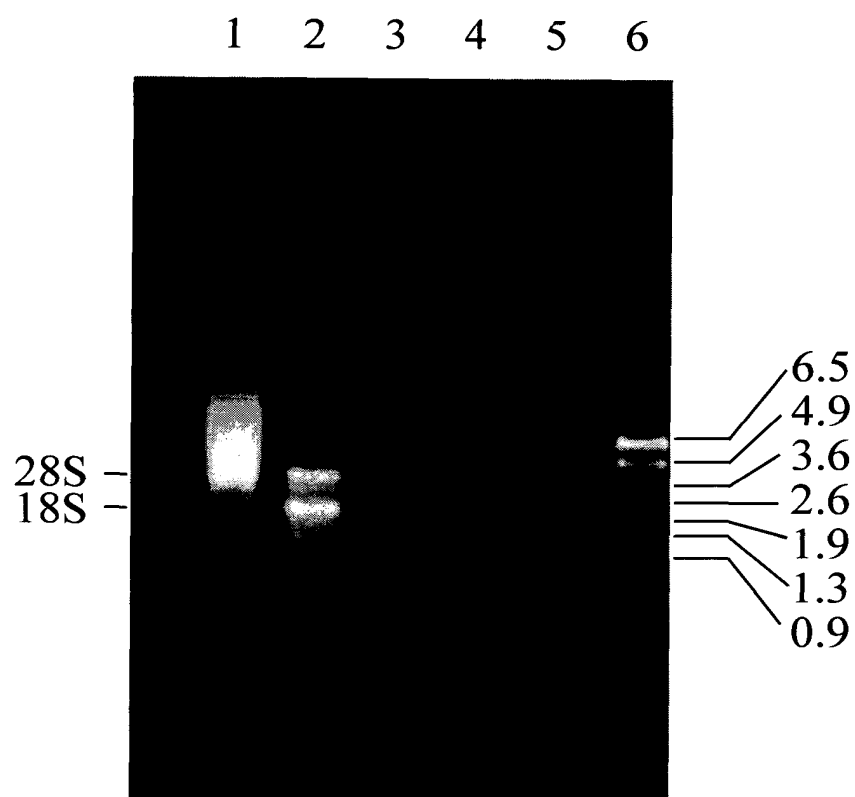


Fig. 2.0

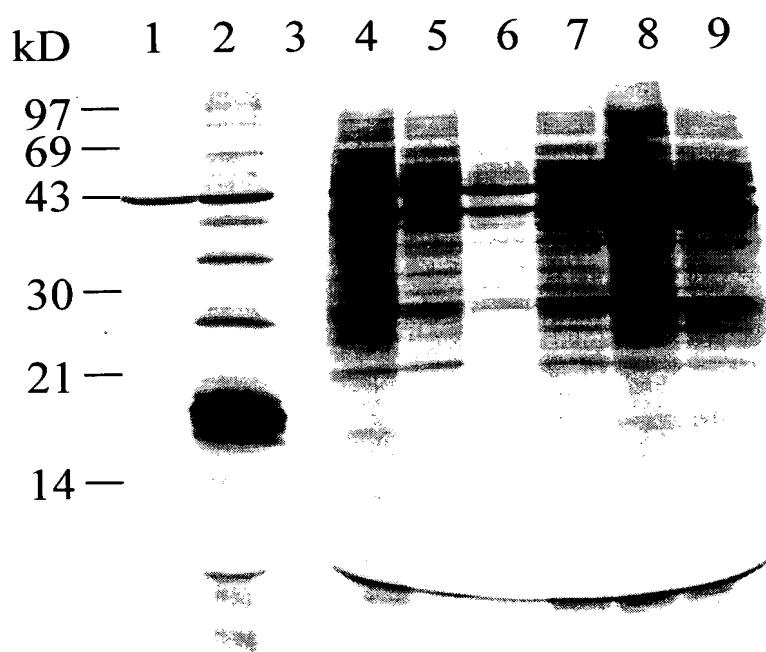


Fig. 2.1

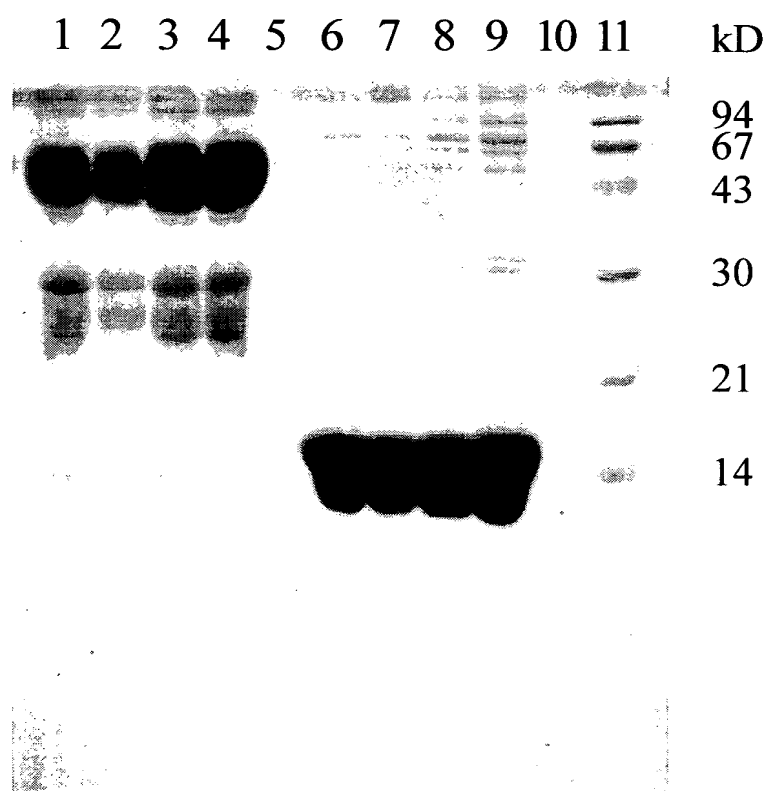


Fig. 2.2

0987543.012302

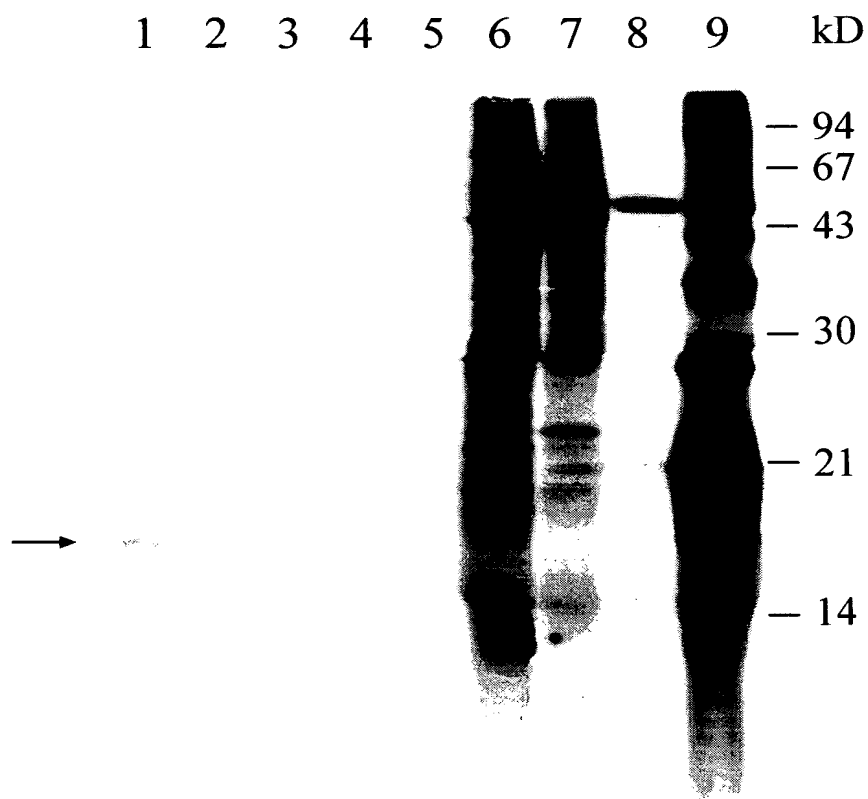


Fig. 2.3

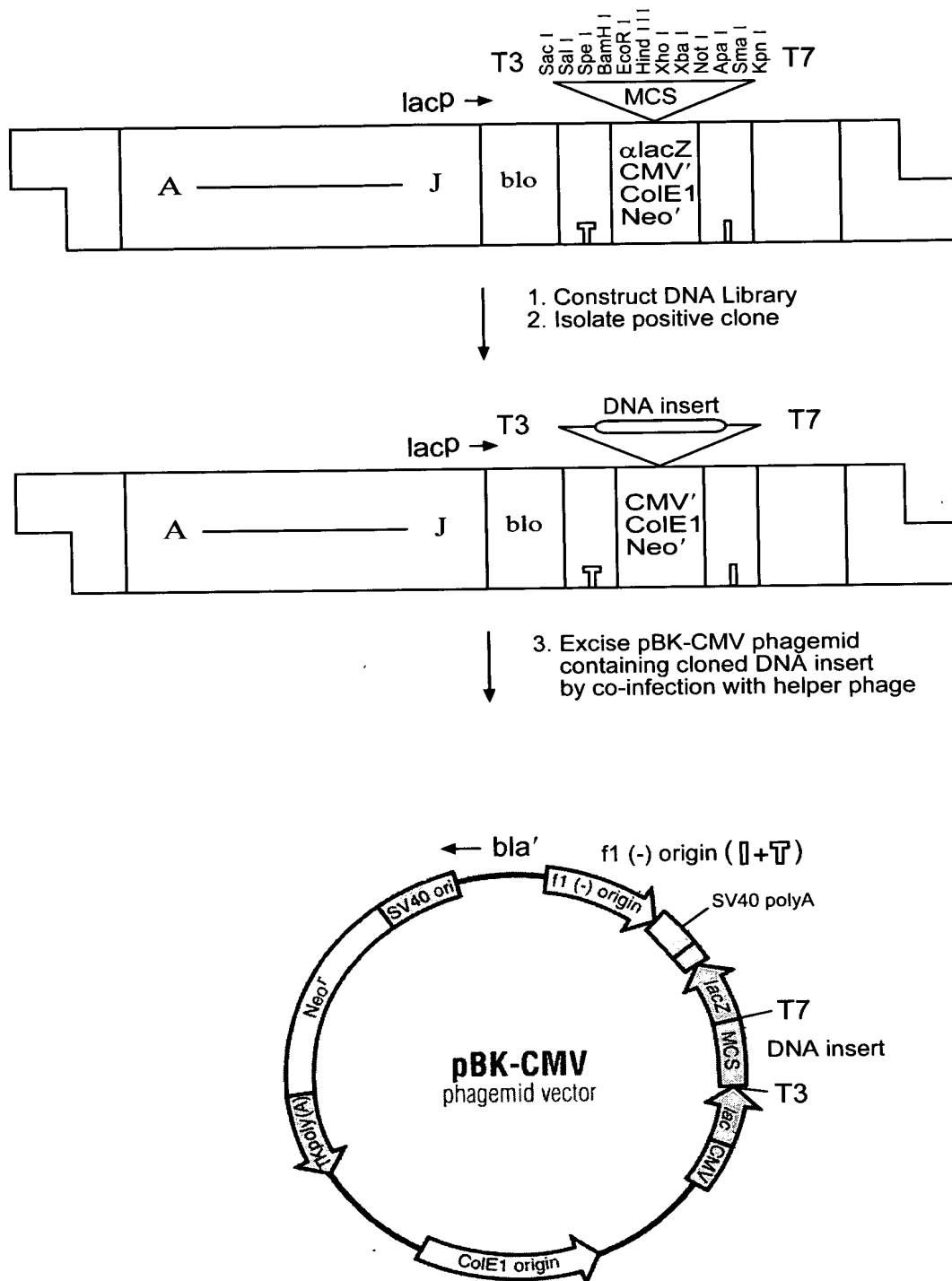


Fig. 2.4a

Fig 2.4b

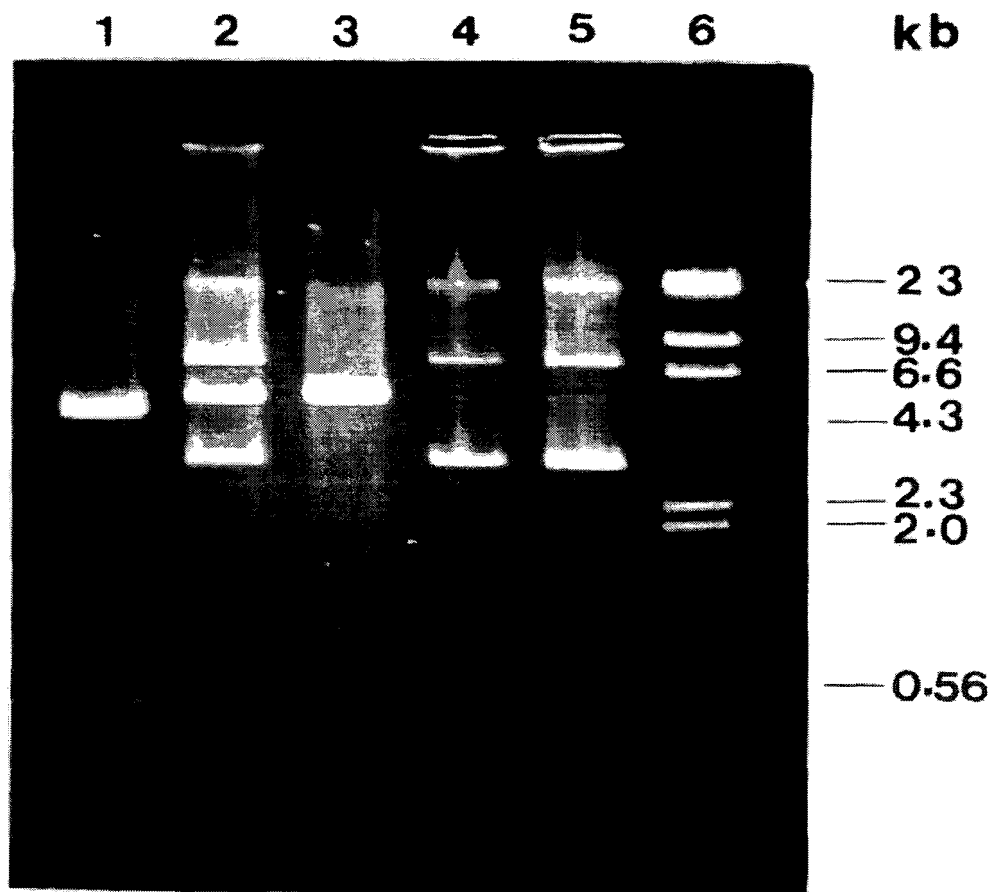


Fig. 2.5

DNA sequence of Tm 13.17 cDNA clone

B E
a c
m o
H R
I I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCACGGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTGGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTCCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

X
h
o
I

481 ATATAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGCGCGCGGCCCATCGTTTTCCACCC

SECRET

cleavage site

M K L L C C L I S L I L L V T V Q A

n-region (basic) h-region (central hydrophobic) c-region (more polar)

Fig. 2.6b

中華民國二十九年十月

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

Fig. 2.6c

1 A O T G O A T C C A A A G A A T T C G O C A C G R G A C T A C T A G A T G A A Tm 13.17
B 1

41 O T T G C T C T G T T O T C T A A T C T C C C T C A T T C T G T T O O T C A C A Tm 13.17
1 C T T A C T T C T C T C A T T C T O T T G O T C C C A B 1

81 O T T C A G O C C C C T G A C C G A O O C A C A A A T T G A O A A A C T O A A C A Tm 13.17
28 O T T C A G O C C C A T A A C T C A O O A A G A R C C T T O A O C T A C T O C C C C B 1

121 A G A T C A G C A A A A A A T O T C A A A A T O A A A G T O O A O T O T C O C A Tm 13.17
68 A A A C C A G C O C A G A O T O C A A O A C T O A A A O T O O A O T O T C C O A B 1

161 A O A O A T C A T A A C C A A A G C T C O C A A C O O T O A C T G O O A O O A C Tm 13.17
118 A O A C O T C A T A A A O A O A O C T C O C A A A A O O T O A C T T O O A O O A C B 1

201 G A T C C C T A A A C T O A A A C O C C A A O T T T T T T O C O T O O C C A O O A Tm 13.17
148 O A C C C C A A A C T O A A A A T O C A A C T T C T T T O C A T T T T C A A O O B 1

241 A C G C C G O T C T G G C C A C G G A A T C G O G A G A G G T G G T G G T C O A Tm 13.17
188 C A C T C O A A A T A G T C G C G O A A T C G O G A G A A A T T O A G G C C O A B 1

281 C O T G T T O A O O O G A G A G O T G A O O A A O O T C A C T G A C A A C G A C Tm 13.17
228 C A C O T T C A A O O O A A O T T O A C O A G O T O A C A A A C G A T O A T B 1

321 G A A O A A A C T O A O A A A A T C A T C A A T A A G T G C O C C O T C A A O A Tm 13.17
268 O A A O A A A O C O A O A A O A T T O T C O A O A A O T C A C G O T O A C T O B 1

361 G A O A T A C T O T T O A A G A O A C G G T O T T C A A T A C T T T T C A A A T O Tm 13.17
308 A A C A C A C T C C G O A A O A T A C G C C A T T T O A A O T T A C C A A A T O B 1

401 T O T C A T O A A A A A C A A O C C A A A O T T C T C A C C A G T T G A T T O A Tm 13.17
348 T O T A T T O A A G A C A A O C C C A A T T T C T C A C C A G T T G A T T O C B 1

441 A C C A C C A C G A C T A G T A G A T G G T T C A A A T G O O T O T G C T T T A C Tm 13.17
388 A G A C T A T T T G T C T G A A A G C T T T G T B 1

481 A T A T A A A A A T A A A O T G T T T C T O A T O T A A A A A A A A A A A A Tm 13.17
428 O C A C A A B 1

81

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSQEIITKARNGDWEDDPKLKRQVFCVARNA	52
	 : . : :. :..	
AFP-3	1	ETPREKCLKQHSACKAESGVSEESLNKVRNREEVDDPKLKEHAFKILKRA	50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTDNDEETEKIINKCAVKRDTVEETVFNTF	102
		: .. . : :.. .. :.. .. :.. :.. : :.. :	
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPOHSSADFF	100
Tm 13.17	103	KCVMKNKP	110
		. : .	
AFP-3	101	KCVHDNRS	108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

Fig. 2.8

Tm 13.17	M	K	L	L	C	C	L	I	S	L	I	L	L	V	T	V	Q	A
AFP-3	M	K	L	L	L	C	L	V	L	V	A	L	V	A	A	T	Y	A
B Protein				L	T	S	L	I	L	L	V	A	V	Q	A			

Fig. 2.9

205270" 01E92B5B

Tm 13.17	NH2-L T	E A	Q I	E	L	N K I S K	K C	Q	N E
		:	:	:					
Tm 12.86	NH2-L T	D E	Q I	Q	R	N K I S K	E ?	Q	Q V

Fig 2.10

09075348 012022

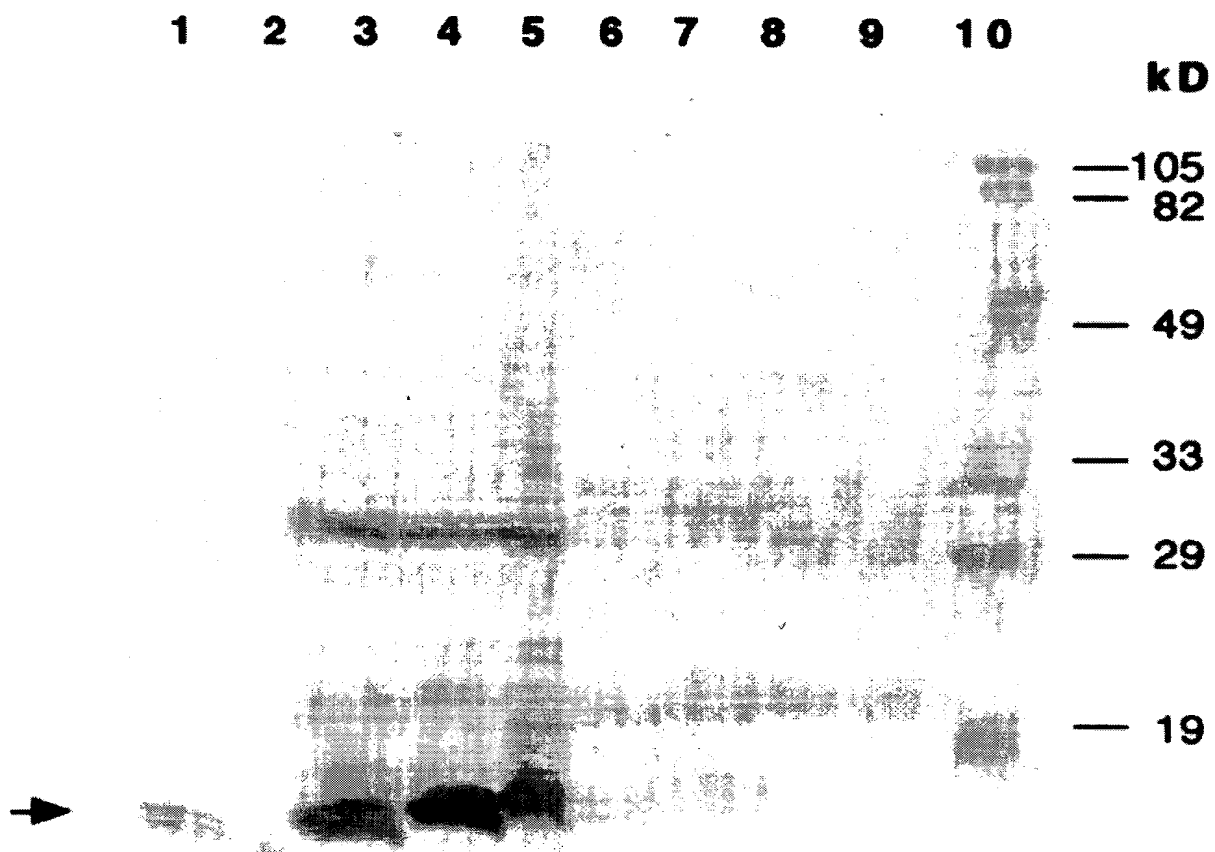


Fig 2.11

Tm 12.86		L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V											
Tm 13.17	1	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	A
B1	13	I	T	E	E	D	L	E	L	L	R	Q	T	S	A	E	C	K	T	E	S	G	V	S	E	D	V	I	K	R	A
AFP-3	1	E	T	P	R	E	K	L	K	Q	H	S	D	A	C	K	A	E	S	G	V	S	E	E	S	L	N	K	V		
Tm13.17	31	R	N	G	D	W	E	D	D	P	K	L	K	R	Q	V	F	C	V	A	R	N	A	G	L	A	T	E	S	G	E
B1	44	R	K	G	D	L	E	D	D	P	K	L	K	M	Q	L	L	C	I	F	K	A	L	E	I	V	A	E	S	G	E
AFP-3	29	R	N	R	E	E	V	D	D	P	K	L	K	E	H	A	F	C	I	L	K	R	A	G	F	I	D	A	S	G	E
Tm13.17	61	V	V	V	D	V	L	R	E	K	V	R	K	V	T	D	N	D	E	E	T	E	K	I	I	N	K	C	A	V	K
B1	75	I	E	A	D	T	F	K	E	K	L	T	R	V	T	N	D	D	E	E	S	E	K	I	V	E	K	C	T	V	T
AFP-3	59	F	Q	L	D	H	I	K	T	K	F	K	E	N	S	E	H	P	E	K	V	D	D	L	V	A	K	C	A	V	K
Tm13.17	91	R	D	T	V	E	E	T	V	F	N	T	F	K	C	V	M	K	N	K	P	K	F	S	P	V	D				
B1	106	E	D	T	P	E	D	T	A	F	E	V	T	K	C	V	L	K	D	K	P	N	F	F	G	D	L	F	V		
AFP-3	89	K	D	T	P	Q	H	S	S	A	D	F	F	K	C	V	H	D	N	R	S										

Fig. 2.12

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCAGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

poly (A) tail

Fig. 3.0

1 GGCACGAGCAAAA ATG AAACTCCTCTTGTGCTTTGCTTTGCGCGCC
 M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
 I V I G A Q A **↑** L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAAGCACGTCTCTGCTTCTCGAAGAAAACCTGGA
 P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
 D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
 I D .

polyadenylation signal

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAA

poly (A) tail

Fig 3.1

Start
↓

2-2	G G C A C G A G C A A A A T G A A A C T C C T C T T G T G C T T T T G C G
2-3	G G C A C G A G C A A A A T G A A A C T C C T C T T G T G C T T T T G C T
2-2	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-3	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-2	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-3	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-2	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-3	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-2	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A T G A T C C C A
2-3	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A C G A T C C C A
2-2	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-3	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-2	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-3	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-2	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-3	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-2	A A G A G G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-3	A A G A A G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-2	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-3	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-2	A A G T G T A T T T A C G A C A G C A A A C C T G A T T T C T C T C C T A
2-3	A A G T G T A T T T A C G A C A G T A A A C C T G A T T T C T C T C C T A
2-2	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-3	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-2	T A A A G G T A A T A T C G T T A T G T A A A A A
2-3	T A A A G G T A C T A T C G T T A T G A A A A A A

Fig 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 3.3

20250428

200210-01E92800

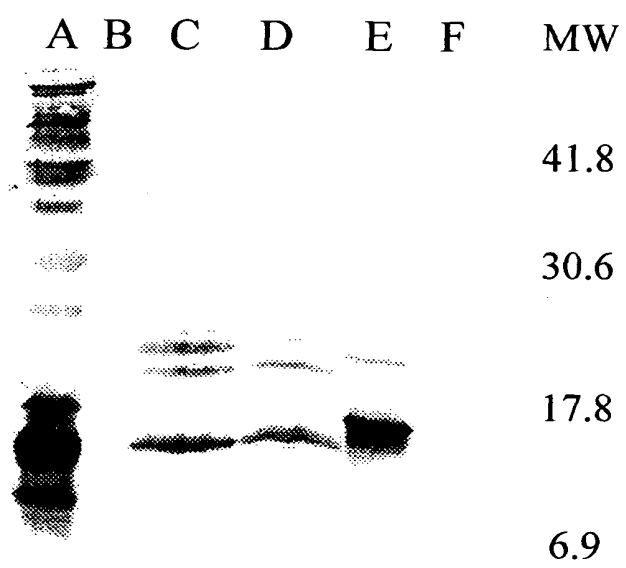
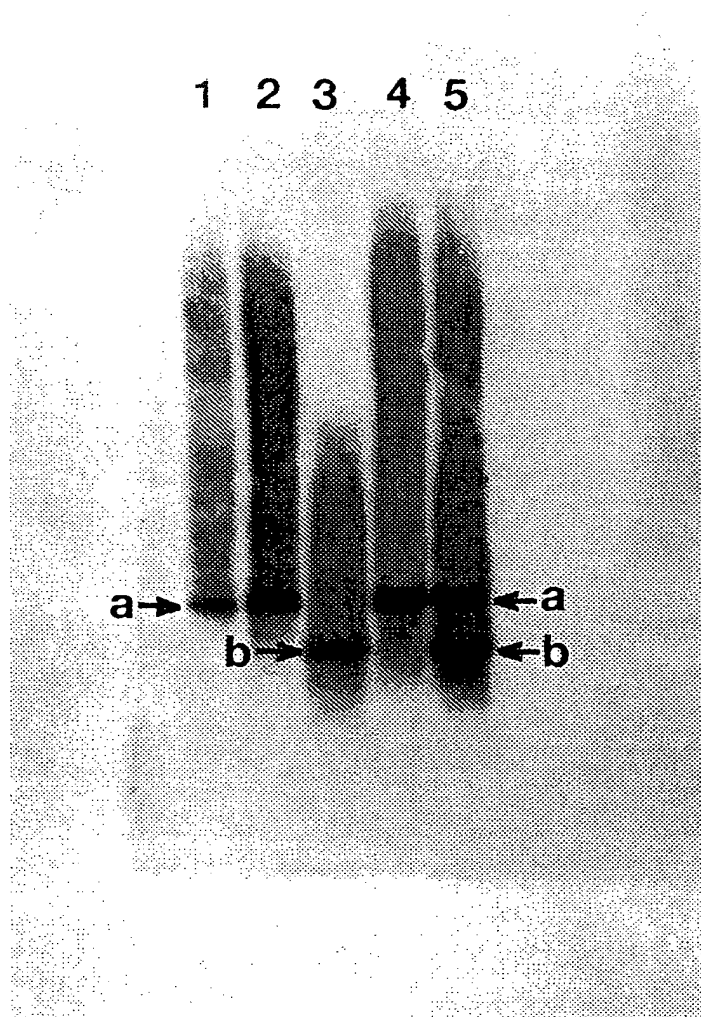


Fig. 3.4

203270" 34E92660

Lane

1 2 3 4 5



577 bp

483 bp

Fig. 4.0

09876543210

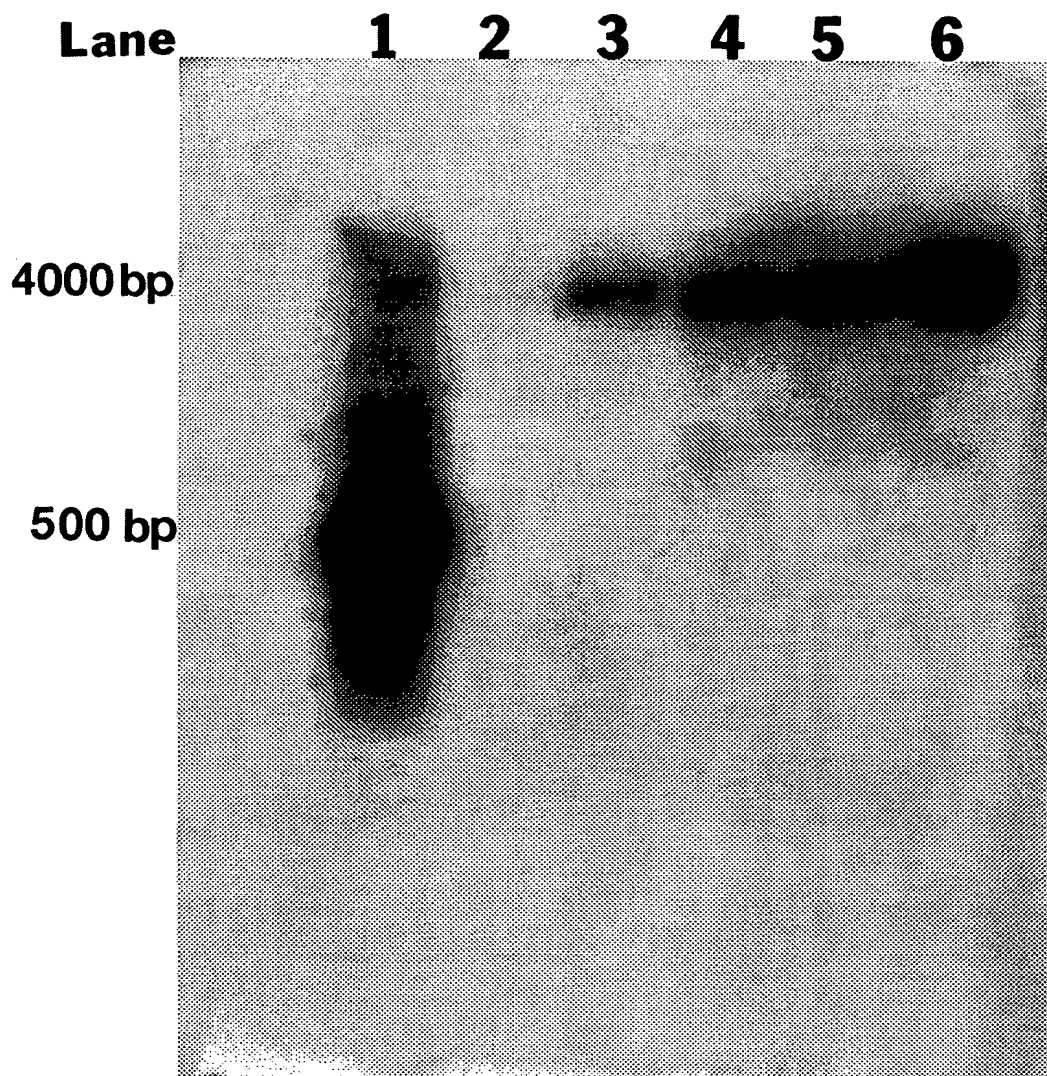


Fig. 4.1

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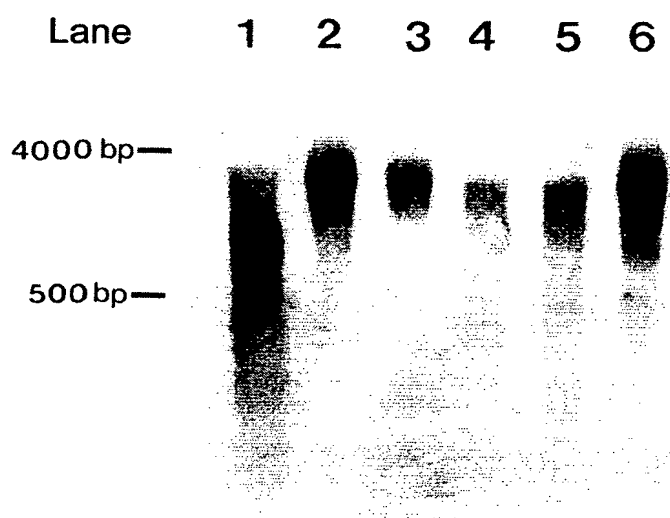
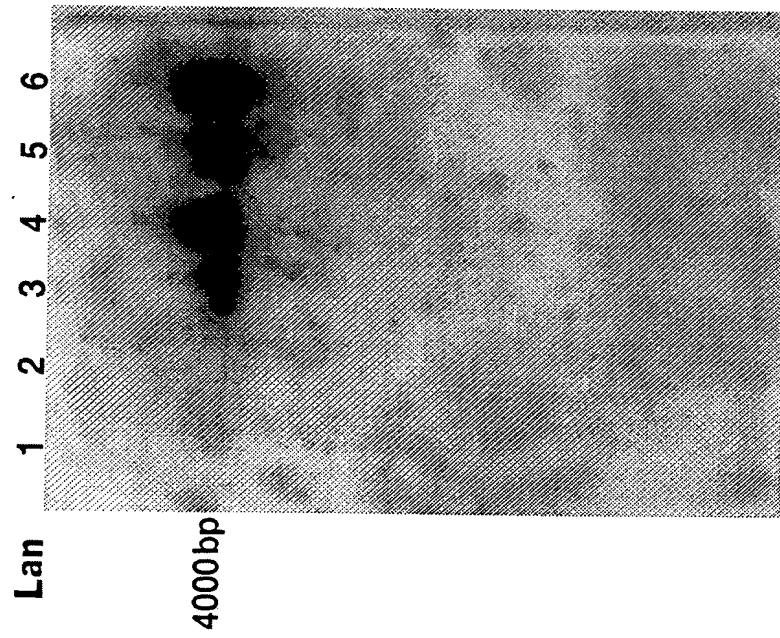


Fig. 4.2

A.



B.

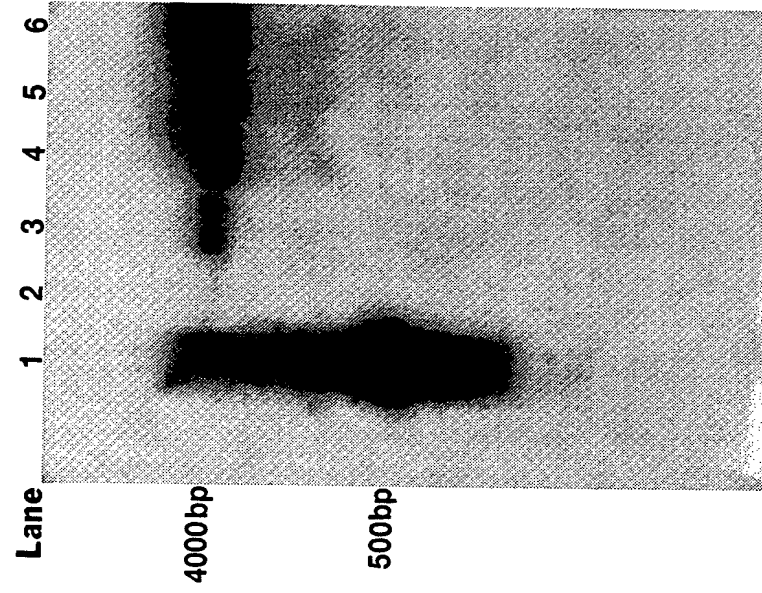


Fig. 4.3

0937349, 043033

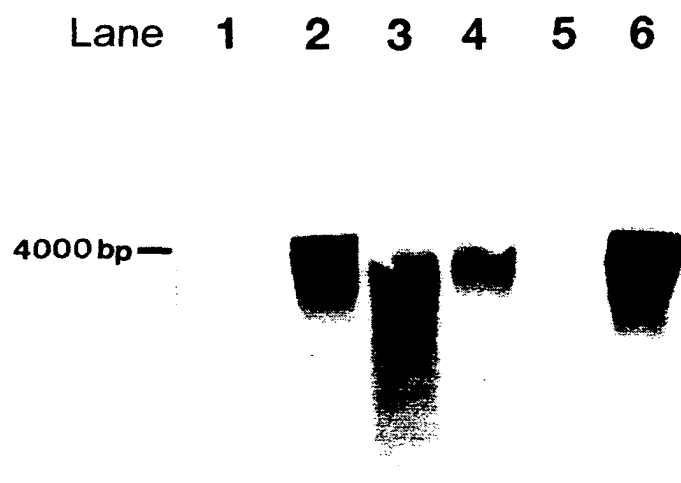


Fig. 4.4

09876343.013602

Lane 1 2 3 4 5



23130

9416

4361

2322

2027

564

Fig. 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAATGAAAGTGGAGTGTCTCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAACTGAAACGCCAAGTTTTTGGCTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCCGGGCCCATCGTTTTCCACCC

Fig. 4.6a

Forward Primer

2-2 L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
T_m 13.17 L T E A Q I E K L N K I S K K C O N E S G V S Q E I I T K A R N G D W E
B2 L T E E D L Q L L R O T S A E C K T E S G A S E A V I K K A R K G D L E
AFP-3 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V R N R E E V

2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H
T_m 13.17 D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K
B2 D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R
AFP-3 D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E

Reverse Primer

2-2 V A S D E E V D K I V Q K C V V K K A T P E E T A Y D T F K C I Y D S
T_m 13.17 V T D N D E E T E K I I N K C A V K R D T V E E T V F N T F K C V M K N
B2 V T N D D E E S E K I V E K C T V T E D T P E D T A F E V T K C V L K D
AFP-3 N S E H P E K V D D L V A K C A V K K D T P Q H S S A D F F K C V H D N

2-2 K P D F S P I D
T_m 13.17 K P K F S P V D
B2 K P N F F G D L F V
AFP-3 R S

Fig. 4.6b

Primer	percent % composition				Melting Temperature (°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

00876349.012803

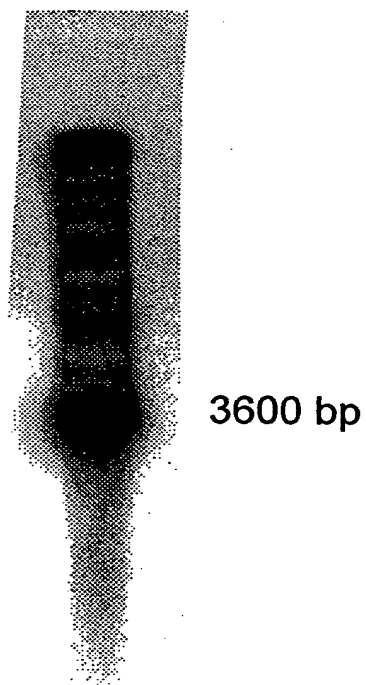


Fig. 4.7

09075349.012002

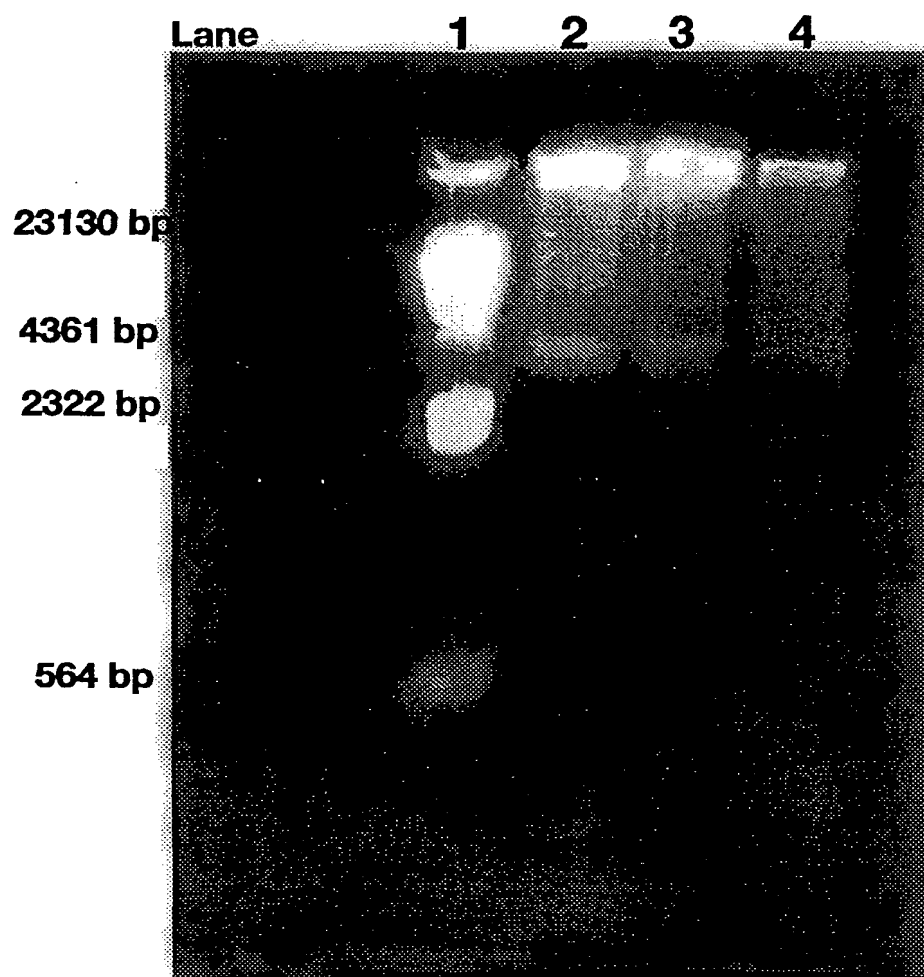


Fig. 4.8

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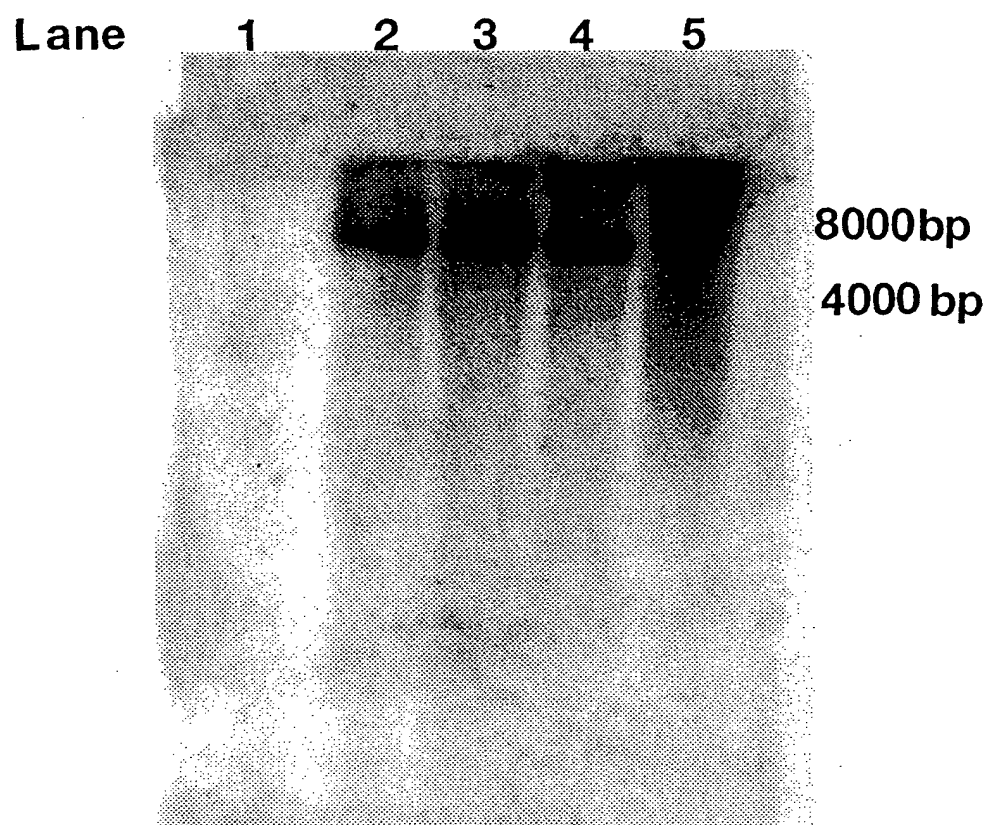


Fig. 4.9

1 GGCACGAGCAAAA ATG GAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D .

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

Fig. 4.10a

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.10b

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTA CTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.11a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.116

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAAGTGGG
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCCTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.12a

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b

THE UNIVERSITY OF CHICAGO

[illegible]

CHART 10 SHEET 2300

2-2 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
 2-3 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
 3-4 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
 3-9 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
 7-5 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V

2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 2-3 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 3-4 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 3-9 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K
 7-5 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D K I V Q K C V V K K

2-2 A T P E E T A Y D T F K C I Y D S K P P D F S P I D *
 2-3 A T P E E T A Y D T F K C I Y D S K P P D F S P I D *
 3-4 A T P E E T A Y D T F K C I Y D S K P P D F S P I D *
 3-9 A T P E E T A Y D T F K C I Y D S K P P D F S P I D *
 7-5 A T P E E T A Y D T F K C I Y D S K P P D F S P I D *

Fig. 4.14

	MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	(% mole)										% most hydrophilic	
	(kDa)	(#)									Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser	Thr	
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3
Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23

Fig. 4.15

→

[illegible][illegible][illegible]

Fig. 4.16

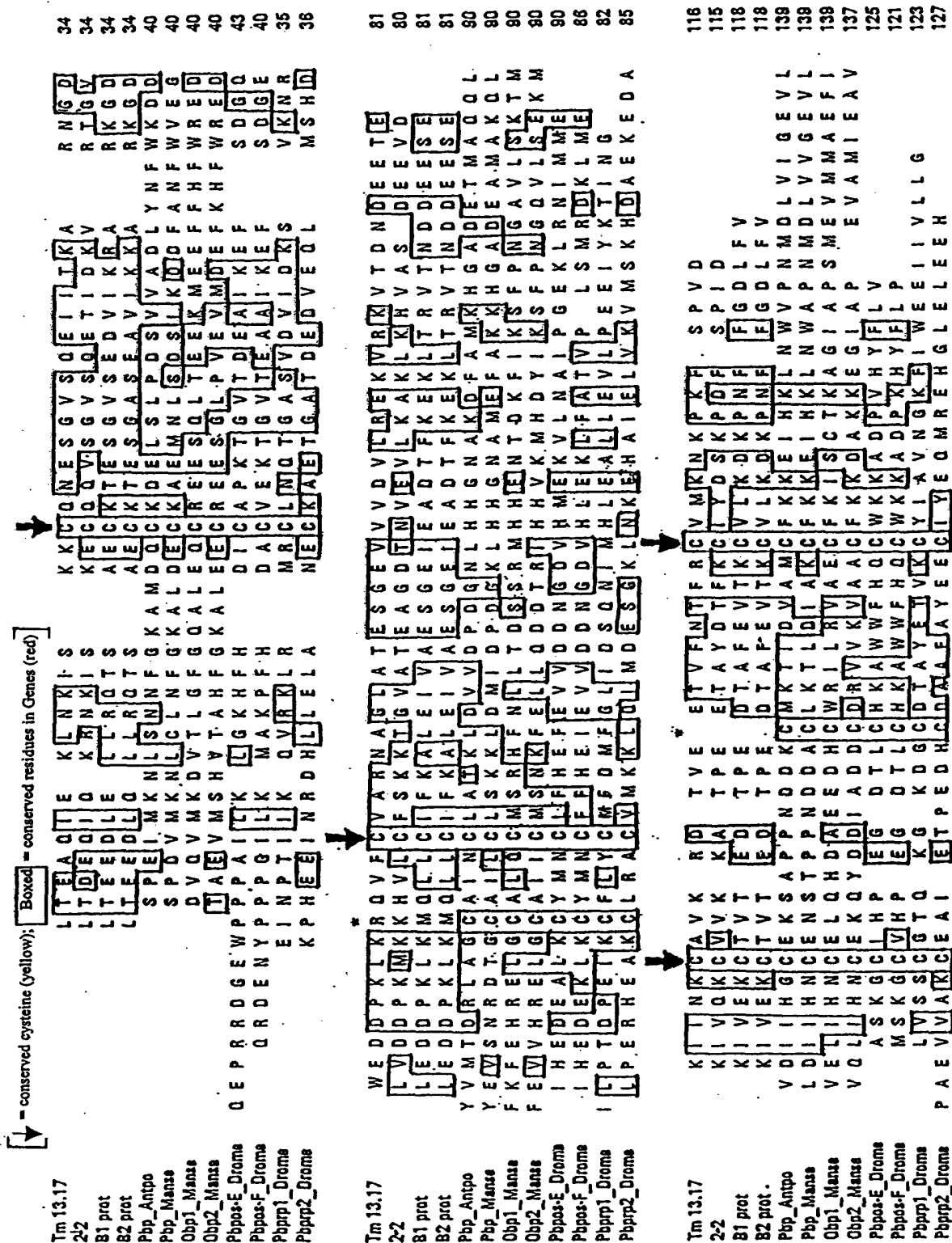


Fig. 4.17

NUCLEOTIDE SEQUENCES

PERCENT SIMILARITY

	1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
	2										2	2-3
	3										3	3-4
	4										4	3-9
	5										5	7-5
	6										6	Tm 13.17
	7										7	B1
	8										8	AFP-3
	9										9	YL-1
	10										10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

AMINO ACID SEQUENCES

PERCENT SIMILARITY

	1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
	2										2	2-3
	3										3	3-4
	4										4	3-9
	5										5	7-5
	6										6	Tm 13.17
	7										7	B1
	8										8	AFP-3
	9										9	YL-1
	10										10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

Fig. 4.19

203210" 84E92860

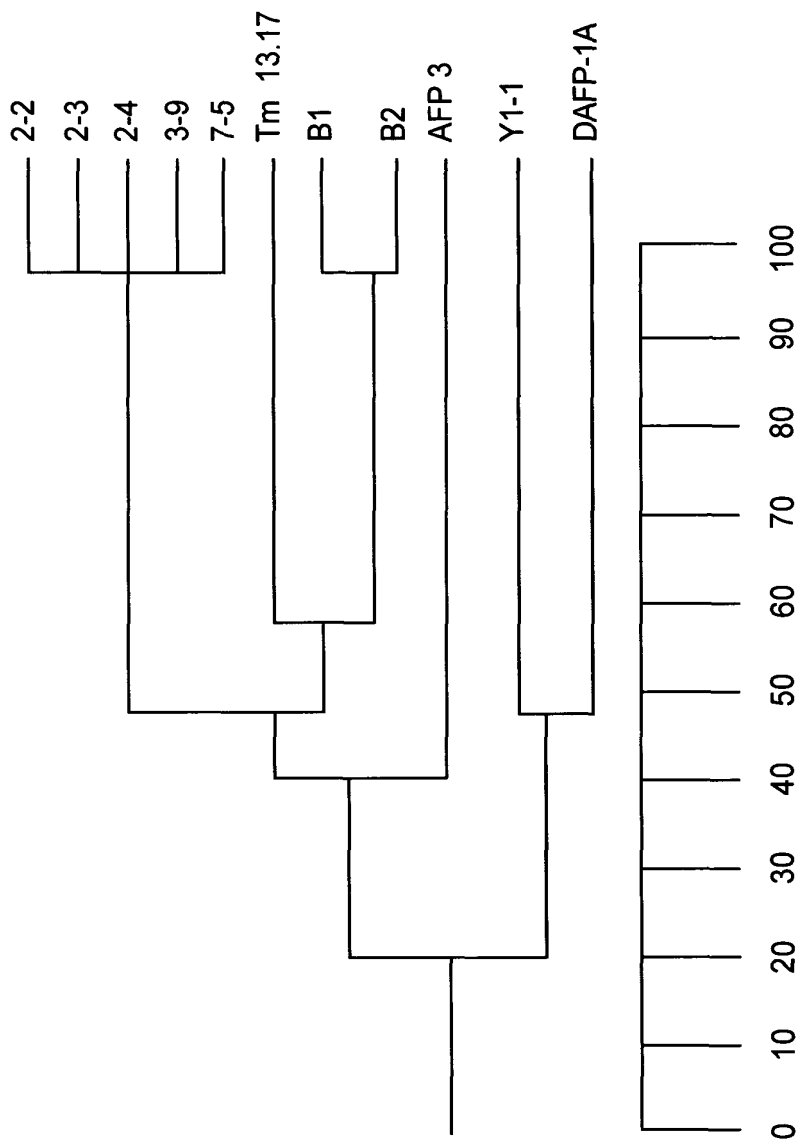


Fig. 4.20

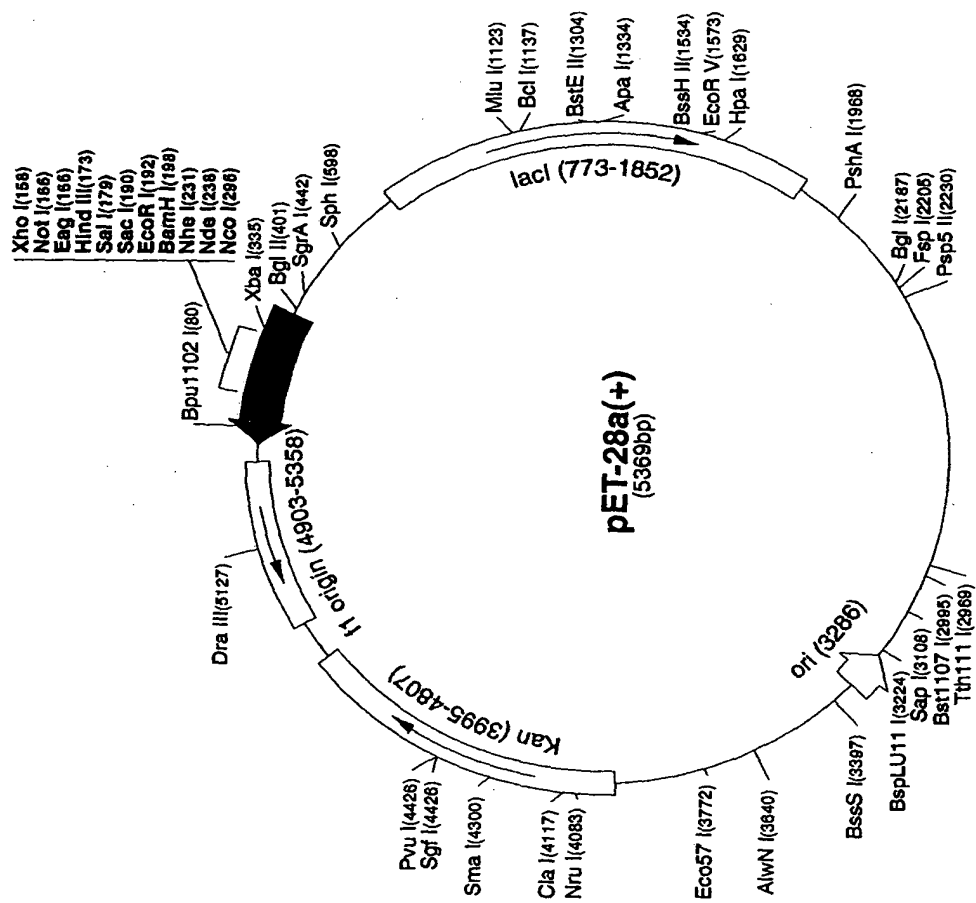


Fig. 5.0

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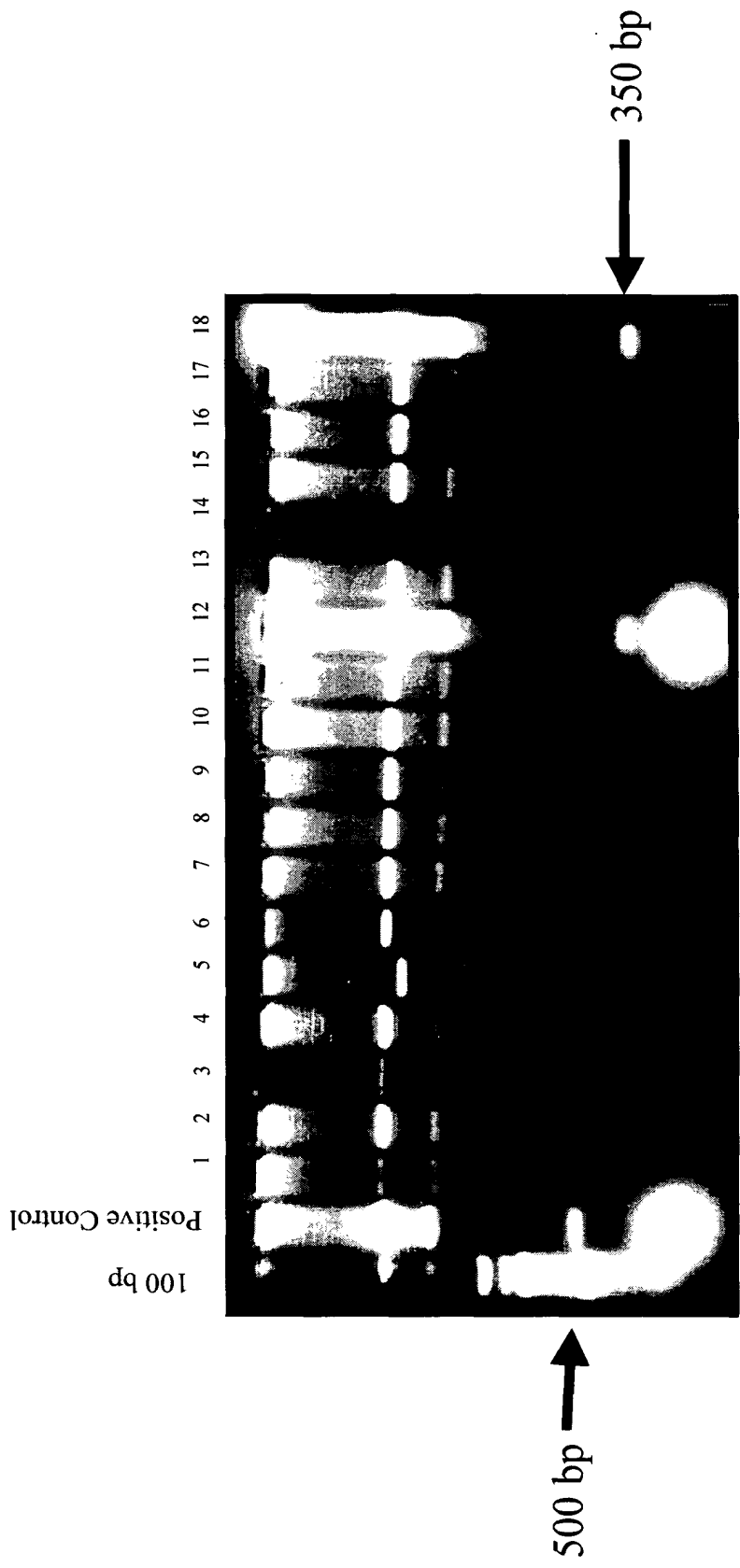


Fig. 5.2

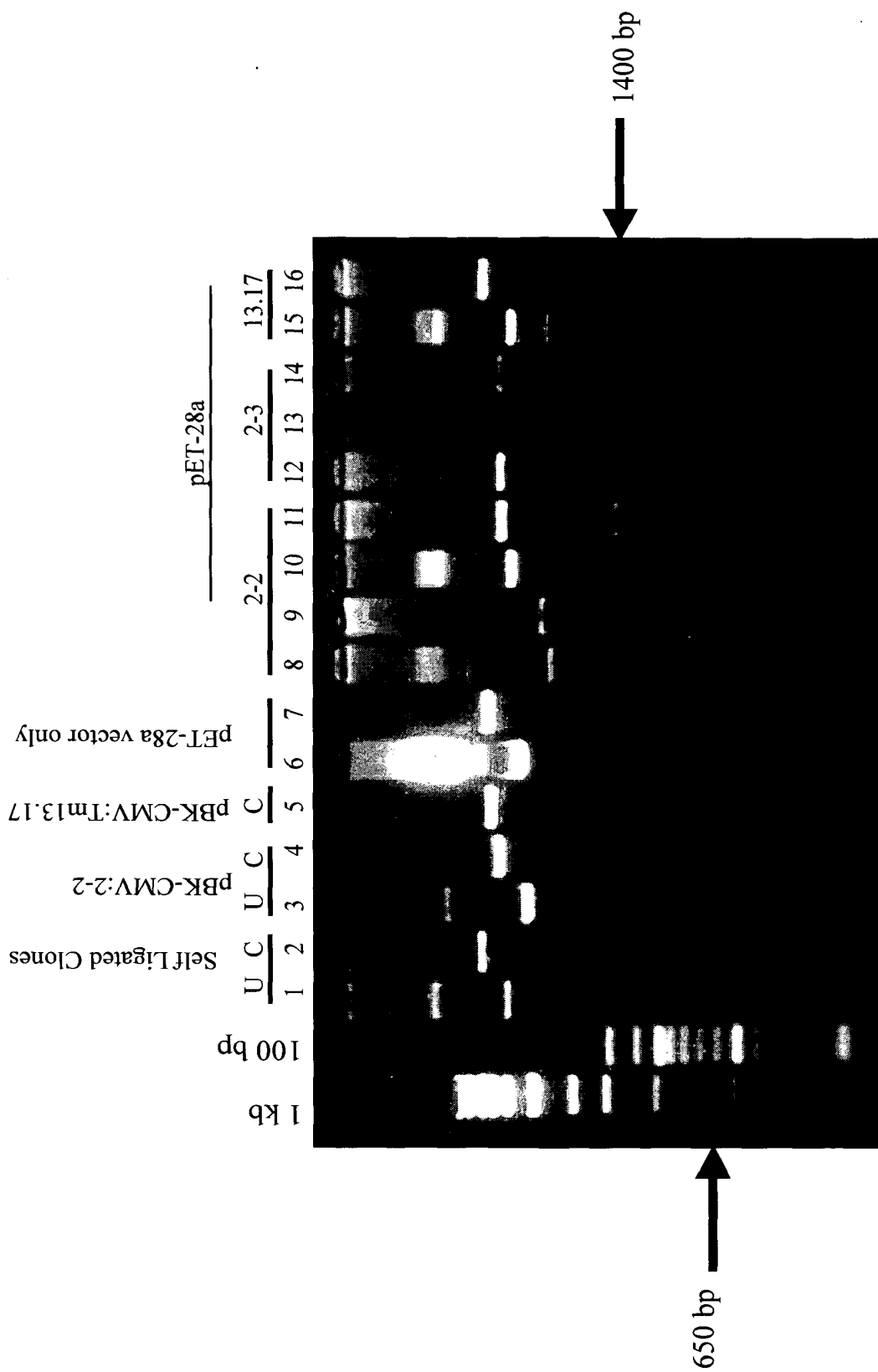


Fig. 5.3

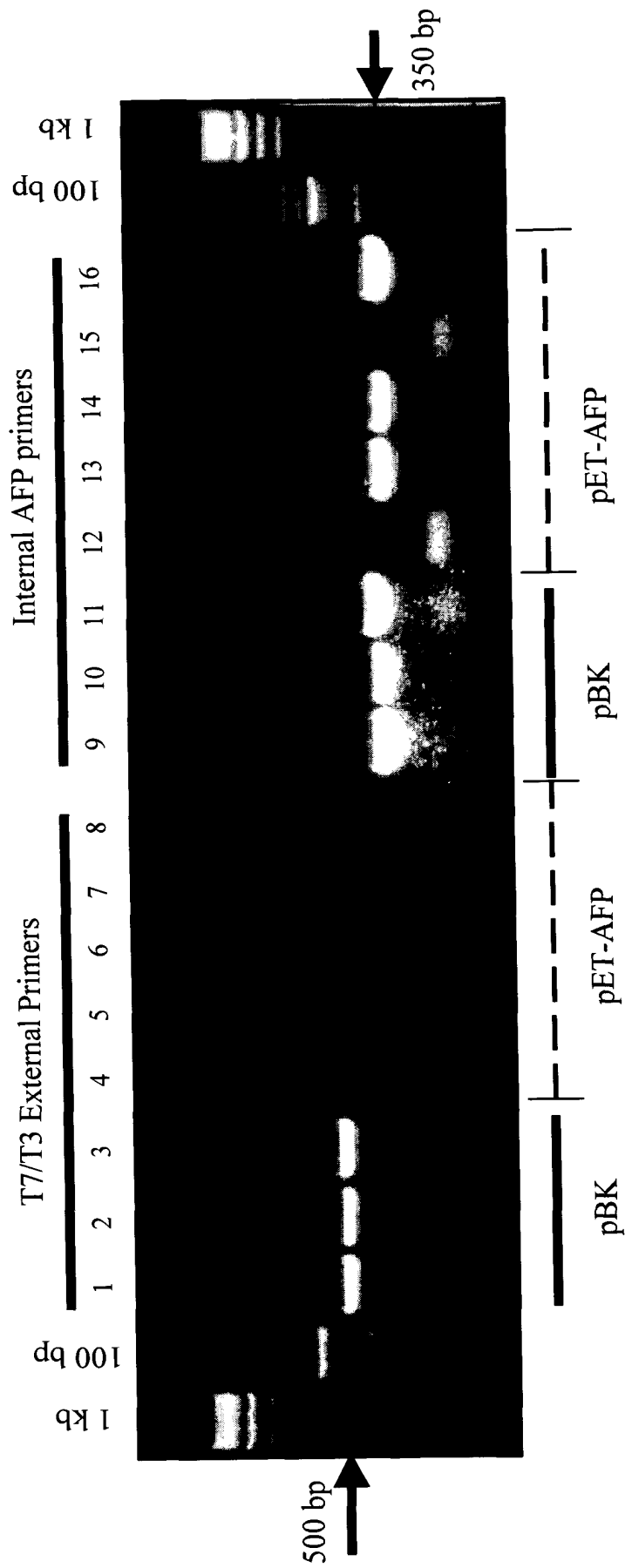


Fig. 5.4

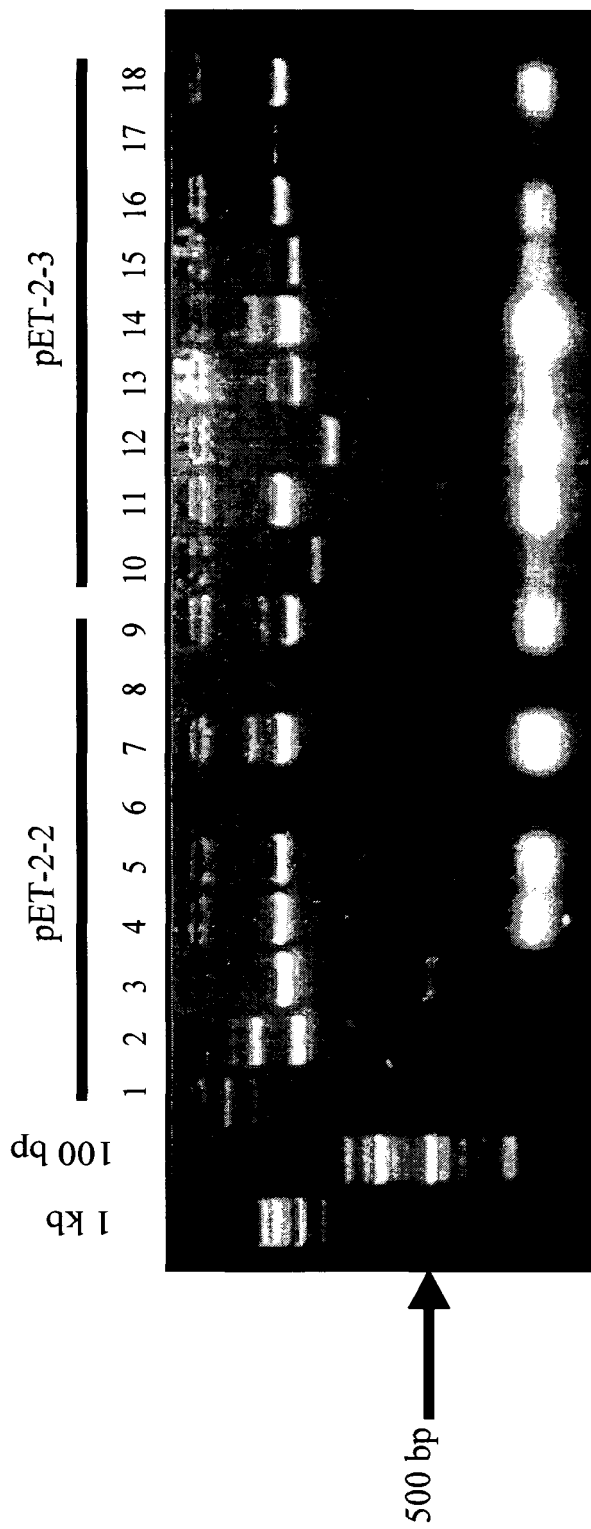


Fig. 5.5

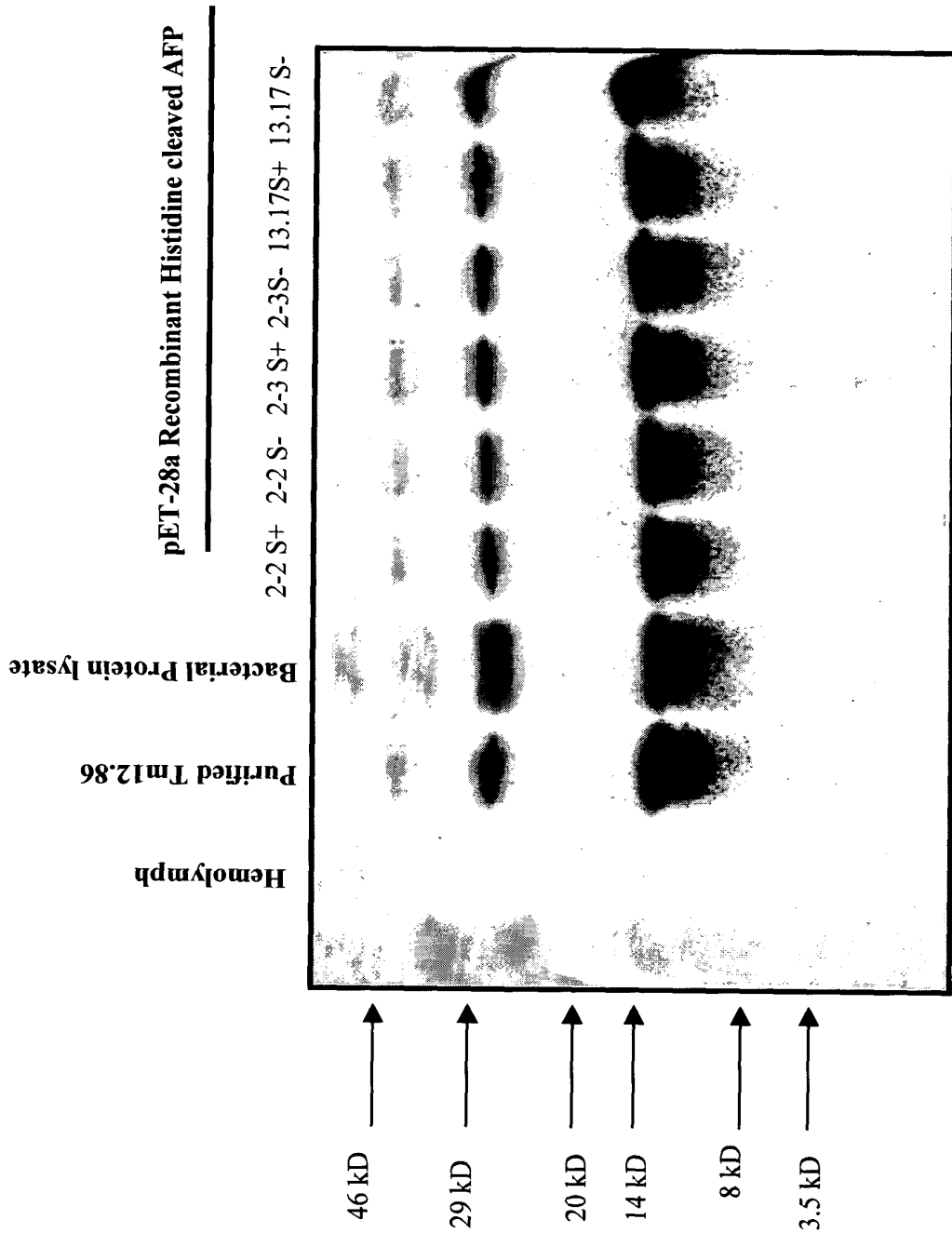


Fig 5.6

THE UNIVERSITY OF CHICAGO

Fig. 5.7

His-tagged clone 2.2 without signal sequence															
TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTTGT	TTACTTTAAG										50	
His-tag Start Codon															
AAGGAGATAT	ACC	ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC		96	
		Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser			
						-30						-25			
AGC	GGC	CTG	GTG	CCG	CGC	GGC	AGC	CAT	ATG	GCT	AGC	ATG	ACT	GGT	141
Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	
			-20					-15					-10		
N-terminal of mature AFP															
GGA	CAG	CAA	ATG	GGT	CGC	GGA	TCC	CTC	ACC	GAC	GAA	CAG	ATA	CAG	186
Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Leu	Thr	Asp	Glu	Gln	Ile	Gln	
			-5					1				5			
AAA	AGG	AAC	AAG	ATC	AGC	AAA	GAA	TGC	CAG	CAG	GTG	TCC	GGA	GTG	231
Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	
		10					15					20			
TCC	CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAT	276
Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	
		25					30					35			
GAT	CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	321
Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	
		40					45					50			
GGA	GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	366
Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	
		55					60					65			
GCC	AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	ATC	411
Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	
		70					75					80			
GTG	CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	456
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	
		85					90					95			
TAT	GAC	ACC	TTC	AAG	TGT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	501
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	
		100					105					110			
Stop Codon															
CCT	ATT	GAT	TAA	CTCGAGCACC	ACCACCACCA	CCACTGAGAT									543
Pro	Ile	Asp	*												
															115

Fig. 5.8

His-tagged clone 2.3 with signal sequence		
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG		50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His His Ser		
-55 -50		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-45 -40 -35		
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met		
-30 -25 -20		
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT		231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala		
-15 -10 -5		
N-terminal of Mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC		276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser		
1 5 10		
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC		321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp		
15 20 25		
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG		366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys		
30 35 40		
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC		411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala		
45 50 55		
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG		456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val		
60 65 70		
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC		501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val		
75 80 85		
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT		546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys		
90 95 100		
Stop Codon		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA		595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *		
105 110 115		
Polyadenylation signal Poly-A tail		
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA		645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT		682

Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

Fig. 5.10

His-tagged Tm 13.17 with signal sequence		
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTAAAG	50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His Ser		
-65	-60	-55
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-50	-45	-40
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile		
-35	-30	-25
AFP Start Codon		
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC		231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser		
-20	-15	-10
N-terminal of mature AFP		
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT		276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile		
-5	1	5
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA		321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly		
10	15	20
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG		366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu		
25	30	35
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC		411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn		
40	45	50
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG		456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu		
55	60	65
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG		501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu		
70	75	80
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG		546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu		
85	90	95
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG		595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys		
100	105	110
Stop Codon		
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG		643
Phe Ser Pro Val Asp *		
115		
Polyadenylation signal Poly-A tail		
TGTGCTTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA		693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT		743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT		777

Fig. 5.11

SECRET

Fig. 5.12

208270" 94292860

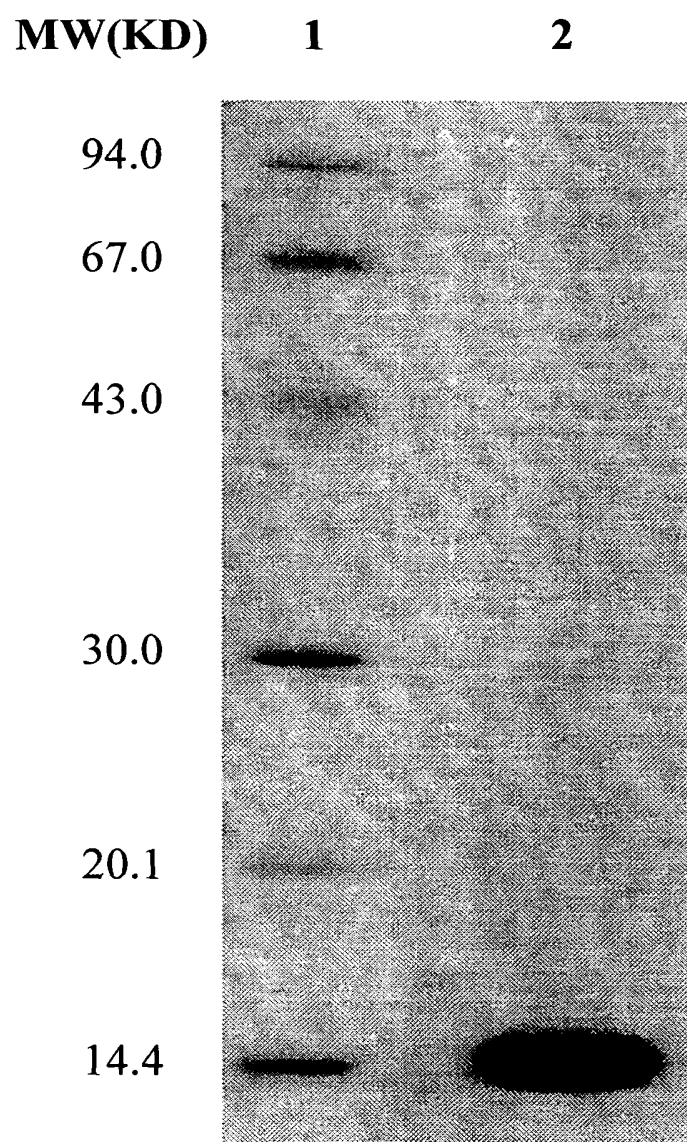


Fig. 6.0

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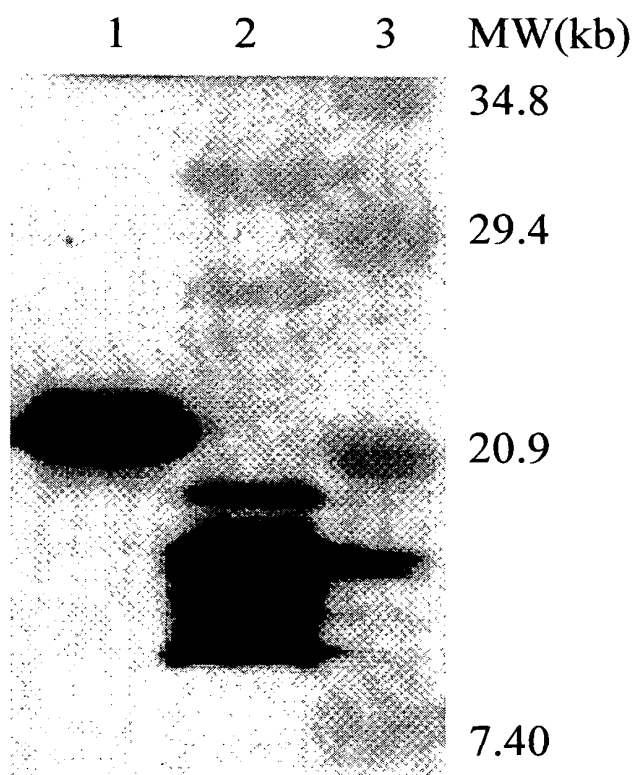


Fig. 6.1

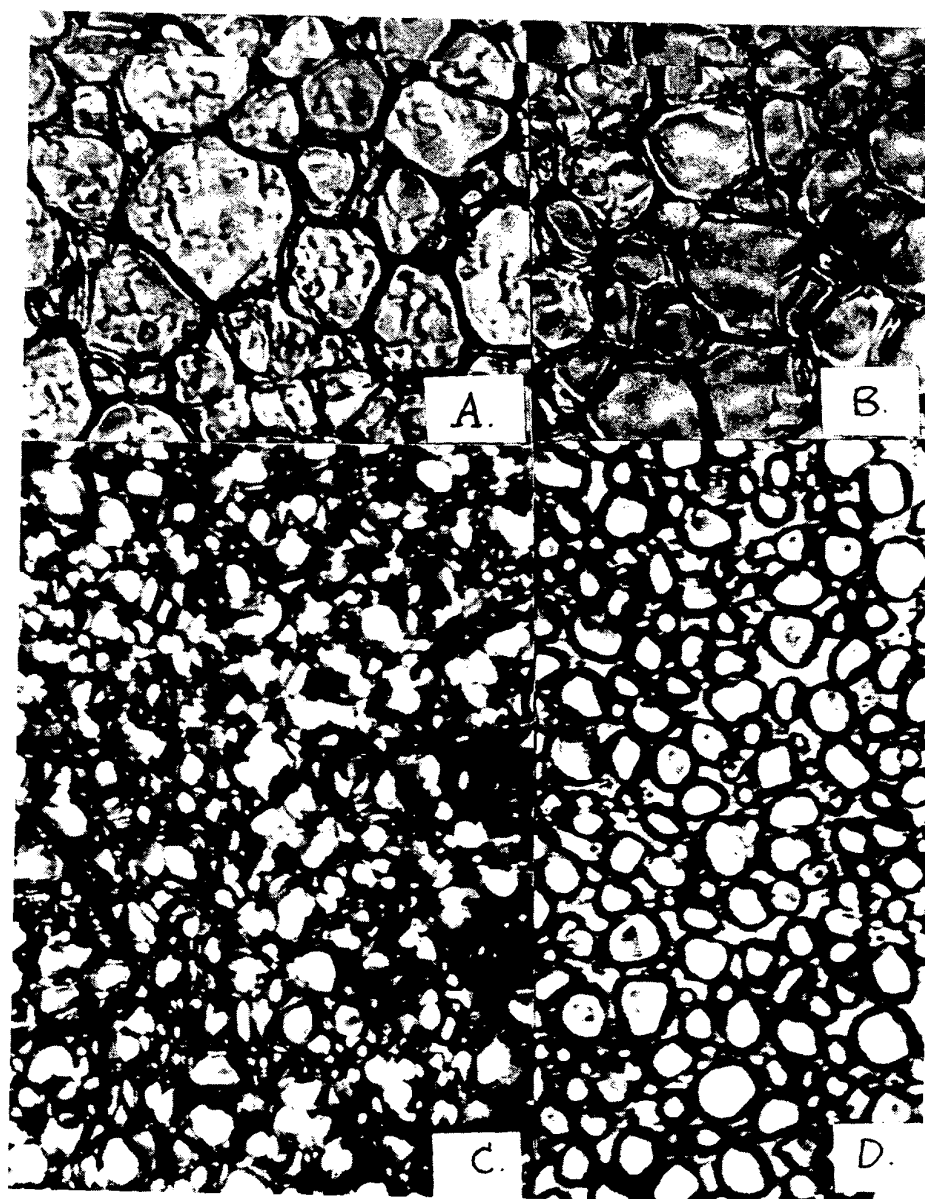


Fig. 6.2

203210" 91592860

Tm 13.17 S-graph data

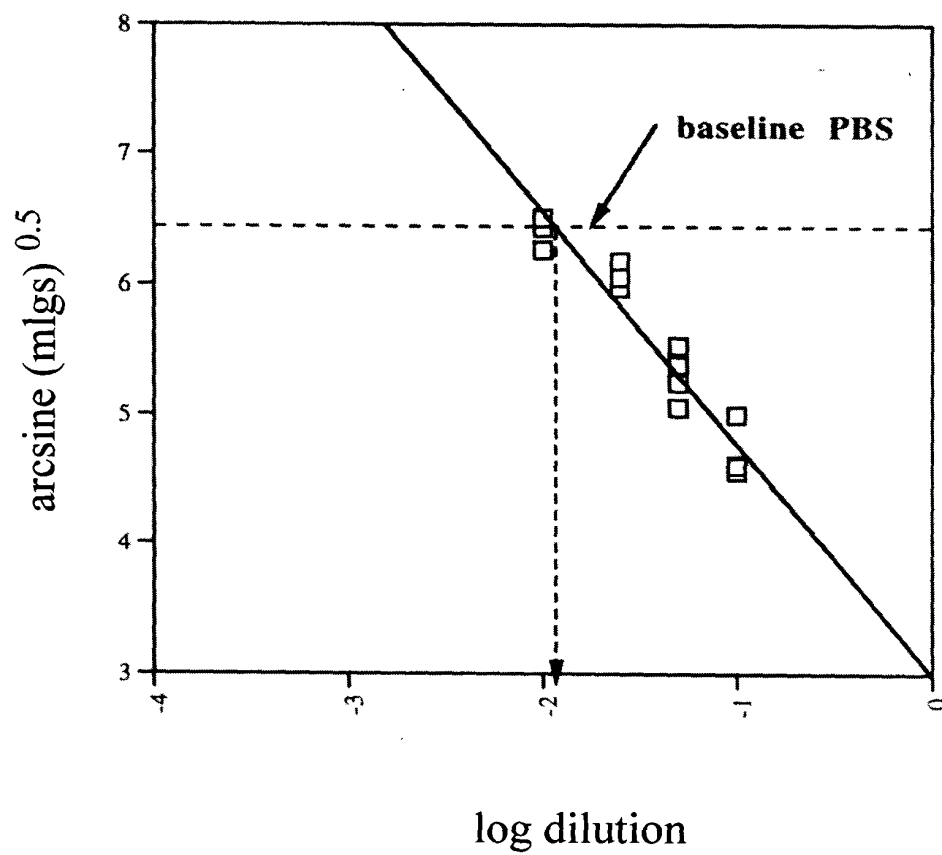


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of Tm12.84	Tm13.17	Consensus with Tm13.17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	A
2	C	C	C	C	C	C	G	N		N	A	N
3	G	G	G	G	G	G	A	R		R	G	R
4	A	A	A	A	A	A	C	N		N	A	N
5	G	G	G	G	G	G	T	N		N	T	N
6	A	A	A	A	A	A	A	N		N	C	N
7	A	A	A	A	A	A	C	N		N	C	N
8	A	A	A	A	A	A	T	N		N	G	N
9	A	A	A	A	A	A	A	A		A	A	A
10	A	A	A	A	A	A	G	R		R	A	R
11	A	A	A	A	A	A						
12									A?	A	A	A
13	A	A	A	A	A	A	T	G	T?	T	T	T
14	T	T	T	T	T	T	G	A	G?	G	G	G
15	G	G	G	G	G	G	A	A		A	A	A
16	A	A	A	A	A	A	A	R		R	C	C
17	A	A	A	A	A	A	G	T		T	T	T
18	A	A	A	A	A	A	T	T		T	C	C
19	C	C	C	C	C	C	C	C		C	C	C
20	T	T	T	T	T	T	T	T		T	T	T
21	C	C	C	C	C	C	C	C		C	C	C
22	C	C	C	C	C	C	T	T		T	T	T
23	T	T	T	T	T	T	T	T		T	T	T
24	T	T	T	T	T	T	T	T		T	T	T
25	T	T	T	T	T	T	T	T		T	T	T
26	T	T	T	T	T	T	T	T		T	T	T
27	G	G	G	G	G	G	T	T		T	T	T
28	T	T	T	T	T	T	T	T		T	T	T
29	G	G	G	G	G	G	T	T		T	T	T
30	C	C	C	C	C	C	T	T		T	T	T
31	T	T	T	T	T	T	T	T		T	T	T
32	T	T	T	T	T	T	T	T		T	T	T
33	T	T	T	T	T	T	T	T		T	T	T
34	G	G	G	G	G	G	A	A		A	T	T
35	C	C	C	C	C	C	T	T		T	T	T
36	G	G	G	G	G	G	C	N		N	T	T
37	T	T	T	T	T	T	T	T		T	T	T
38	T	T	T	T	T	T	T	T		T	T	T
39	C	C	C	C	C	C	C	C		C	T	T
40	C	C	C	C	C	C	C	C		C	T	T
41	C	C	C	C	C	C	C	C		C	T	T
42	C	C	C	C	C	C	C	C		C	T	T
43	C	C	C	C	C	C	C	C		C	T	T
44	C	C	C	C	C	C	C	C		C	T	T
45	C	C	C	C	C	C	C	C		C	T	T
46	C	C	C	C	C	C	C	C		C	T	T
47	A	A	A	A	A	A	T	T		T	T	T
48	T	T	T	T	T	T	T	T		T	T	T
49	C	C	C	C	C	C	T	T		T	T	T
50	T	T	T	T	T	T	T	T		T	T	T
51	C	C	C	C	C	C	T	T		T	T	T
52	A	A	A	A	A	A	T	T		T	T	T
53	T	T	T	T	T	T	T	T		T	T	T
54	C	C	C	C	C	C	T	T		T	T	T
55	G	G	G	G	G	G	G	G		G	T	T
56	A	A	A	A	A	A	A	A		A	T	T
57	G	G	G	G	G	G	A	A		A	T	T
58	C	C	C	C	C	C	C	C		C	T	T
59	C	C	C	C	C	C	C	C		C	T	T
60	T	T	T	T	T	T	T	T		T	T	T
61	C	C	C	C	C	C	A	A		A	T	T
62	A	A	A	A	A	A	A	A		A	T	T
63	G	G	G	G	G	G	G	G		G	T	T
64	C	C	C	C	C	C	C	C		C	T	T
65	T	T	T	T	T	T	T	T		T	T	T
66	C	C	C	C	C	C	T	T		T	T	T
67	T	T	T	T	T	T	T	T		T	T	T
68	C	C	C	C	C	C	T	T		T	T	T
69	C	C	C	C	C	C	T	T		T	T	T
70	A	A	A	A	A	A	A	A		A	T	T
71	C	C	C	C	C	C	C	C		C	T	T
72	C	C	C	C	C	C	G	G		G	T	T
73	G	G	G	G	G	G	A	A		A	T	T
74	A	A	A	A	A	A	C	C		C	T	T
75	A	A	A	A	A	A	G	G		G	T	T
76	A	A	A	A	A	A	A	A		A	T	T
77	A	A	A	A	A	A	A	A		A	T	T
78	A	A	A	A	A	A	A	A		A	T	T
79	A	A	A	A	A	A	C	C		C	T	T
80	A	A	A	A	A	A	A	A		A	T	T
81	G	G	G	G	G	G	A	A		A	T	T
82	A	A	A	A	A	A	T	T		T	T	T
83	T	T	T	T	T	T	A	A		A	T	T
84	A	A	A	A	A	A	A	A		A	T	T
85	C	C	C	C	C	C	A	A		A	T	T
86	A	A	A	A	A	A	A	A		A	T	T
87	G	G	G	G	G	G	A	A		A	T	T
88	A	A	A	A	A	A	A	A		A	T	T
89	A	A	A	A	A	A	A	A		A	T	T
90	A	A	A	A	A	A	A	A		A	T	T
91	A	A	A	A	A	A	A	A		A	T	T
92	G	G	G	G	G	G	T	T		T	T	T
93	A	A	A	A	A	A	G	G		G	T	T
94	A	A	A	A	A	A	A	A		A	T	T
95	C	C	C	C	C	C	A	A		A	T	T
96	A	A	A	A	A	A	A	A		A	T	T
97	A	A	A	A	A	A	A	A		A	T	T
98	A	A	A	A	A	A	A	A		A	T	T
99	A	A	A	A	A	A	A	A		A	T	T
100	T	T	T	T	T	T	T	T		T	T	T
101	A	A	A	A	A	A	T	T		T	T	T
102	C	C	C	C	C	C	C	C		C	T	T
103	A	A	A	A	A	A	C	C		C	T	T
104	G	G	G	G	G	G	G	G		G	T	T
105	C	C	C	C	C	C	A	A		A	T	T
106	A	A	A	A	A	A	A	A		A	T	T
107	A	A	A	A	A	A	A	A		A	T	T
108	A	A	A	A	A	A	A	A		A	T	T
109	A	A	A	A	A	A	A	A		A	T	T
110	A	A	A	A	A	A	A	A		A	T	T
111	T	T	T	T	T	T	T	T		T	T	T
112	G	G	G	G	G	G	T	T		T	T	T
113	C	C	C	C	C	C	C	C		C	T	T
114	C	C	C	C	C	C	C	C		C	T	T
115	A	A	A	A	A	A	A	A		A	T	T
116	A	A	A	A	A	A	A	A		A	T	T
117	A	A	A	A	A	A	A	A		A	T	T

Fig. 7.2

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	A	H	A	N	C	N
119	A	A	A	A	A	A	T	A	C	N	T	N
120	G	G	G	G	G	G	G	A	T	N	T	N
121	T	T	T	T	T	T/A	A	A	G	A	G	A
122	G	G	G	G	G	G	A	T/A	A	A	T	T/A
123	T	T	T	T	T	T	A	C/G	G	A	C	C/G
124	C	C	C	C	C	C	T	Y	T	Y	T	Y
125	C	C	C	C	C	C	G	G	G	G	G	G
126	G	G	G	G	G	G	A	G	A	A	A	A
127	G	G	G	G	G	G	T	G	G	G	G	G
128	A	A	A	A	A	A	G	T	T	T	T	T
129	G	G	G	G	G	G	T	T	T	T	T	T
130	T	T	T	T	T	T	G	T	T	T	T	T
131	G	G	G	G	G	G	T	C	T	C	T	C
132	T	T	T	T	T	T	C	C	C	C	C	C
133	C	C	C	C	C	C	G	C/G	C	C/G	G	N
134	C	C	C	C	C	C	C	C	G	C/G	A	C/G
135	C	C	C	C	C	C	A	A	A	A	A	A
136	C	C	C	C	C	C	A	A	A	A	A	A
137	A	A	A	A	A	A	G	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	G	G	G	G	G	G	A	A	A	A	A	A
140	A	A	A	A	A	A	G	A	C	G/C	G	G/C
141	A	A	A	A	A	A	A	A	G	R	T	N
142	A	A	A	A	A	A	G	Y	T	Y	C	Y
143	C	C	C	C	C	C	C	G/C	C	G/C	C	C
144	G	G	G	G	G	G	A	A	A	A	A	A
145	A	A	A	A	A	A	T	A	T	T	T	T
146	T	T	T	T	T	T	A	T	A	A	A	A
147	C	C	C	C	C	C	A	N	A	N	A	A
148	G	G	G	G	G	G	A	N	A	N	A	A
149	A	A	A	A	A	A	C	N	A	N	A	A
150	C	C	C	C	C	C	C	A	A	C/G	A	C/G
151	A	A	A	A	A	A	A	A	A	R	A	R
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	G	A	G	A	G	R
154	G	G	G	G	G	G	T	G	T	Y	T	Y
155	T	T	T	T	T	T	C	Y	T	C	C	C
156	C	C	C	C	C	C	C	C	C	C	C	C
157	C	C	C	C	C	C	C	C	C	C	C	C
158	G	G	G	G	G	G	C	C	C	C	C	C
159	C	C	C	C	C	C	A	A	A	A	A	A
160	A	A	A	A	A	A	A	A	A	A	A	A
161	A	A	A	A	A	A	C	A	A	N	A	N
162	A	A	A	A	A	A	C	A	A	N	A	N
163	G	G	G	G	G	G	G	G	G	G	G	G/C
164	T	T	T	T	T	T	T	T	T	T	T	T
165	G	G	G	G	G	G	G	T	G	A	G	G
166	T	T	T	T	T	T	A	T/A	T/A	T/A	T/A	T/A
167	C	C	C	C	C	C	C	C	C	C	C	C
168	T	T	T	T	T	T	T	N	T	N	N	N
169	T	T	T	T	T	T	G	G	G	G	G	G
170	T	T	T	T	T	T	G	N	T	N	N	N
171	G	G	G	G	G	G	G	G	G	G	G	G
172	T	T	T	T	T	T	A	T/A	A	T/A	T/A	T/A
173	C	C	C	C	C	C	G	C/G	C/G	C/G	C/G	C/G
174	G	G	G	G	G	G	A	G	A	G	A	A
175	A	A	A	A	A	A	C	A	C	A	A	A
176	T	T	T	T	T	T	G	A	G	A	A	A
177	G	G	G	G	G	G	C	C	C	C	C	C
178	A	A	A	A	A	A	A	A	A	A	A	A
179	T	T	T	T	T	T	C	T	C	C	C	C
180	C	C	C	C	C	C	C	C	C	C	C	C
181	C	C	C	C	C	C	C	C	C	C	C	C
182	C	C	C	C	C	C	C	C	C	C	C	C
183	A	A	A	A	A	A	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	T	T	T	T	T	T	G	N	C	N	C	N
189	G	G	G	G	G	G	A	T	A	T	A	T
190	A	A	A	A	A	A	A	A	A	A	A	A
191	A	A	A	A	A	A	A	A	A	A	A	A
192	G	G	G	G	G	G	A	R	A	R	A	R
193	A	A	A	A	A	A	C	N	A	N	A	N
194	A	A	A	A	A	A	C	R	A	R	A	R
195	G	G	G	G	G	G	C	G/C	G	G/C	G	G/C
196	C	C	C	C	C	C	C	C	C	C	C	C
197	A	A	A	A	A	A	A	A	A	A	A	A
198	C	C	C	C	C	C	A	A	A	A	A	A
199	G	G	G	G	G	G	G	N	A	N	A	N
200	T	T	T	T	T	T	T	T	T	T	T	T
201	C	C	C	C	C	C	T	Y	C	Y	C	Y
202	C	C	C	C	C	C	T	Y	T	Y	T	Y
203	T	T	T	T	T	T	T	Y	T	Y	T	Y
204	C	C	C	C	C	C	T	Y	T	Y	T	Y
205	T	T	T	T	T	T	G	C	C	C	C	C
206	G	G	G	G	G	G	C	N	A	N	A	N
207	C	C	C	C	C	C	T	T	T	T	T	T
208	T	T	T	T	T	T	T	C/G	T	N	T	N
209	C	C	C	C	C	C	C	N	T	N	T	N
210	T	T	T	T	T	T	C	C	T	C	T	C
211	C	C	C	C	C	C	G	G/C	T	G/C	G	G/C
212	G	G	G	G	G	G	A	A	A	A	A	A
213	A	A	A	A	A	A	A	R	A	R	A	R
214	A	A	A	A	A	A	G	G	A	G	A	G
215	A	A	A	A	A	A	A	A	A	A	A	A
216	G	G	G	G	G	G	A	R	A	R	A	R
217	A	A	A	A	A	A	A	N	A	N	A	N
218	A	A	A	A	A	A	C	C	A	C	A	C
219	A	A	A	A	A	A	C	C	A	C	A	C
220	C	C	C	C	C	C	C	C	C	C	C	C
221	T	T	T	T	T	T	G	G	A	A	A	A
222	G	G	G	G	G	G	A	G	A	A	A	A
223	A	A	A	A	A	A	T	G	A	A	A	A
224	G	G	G	G	G	G	G	A	A	A	A	A
225	A	A	A	A	A	A	T	G/C	A	N	T	N
226	G	G	G	G	G	G	C	T	A	A	T	A
227	T	T	T	T	T	T	G	G	A	A	T	A
228	G	G	G	G	G	G	C	C	A	A	T	A
229	C	C	C	C	C	C	C	N	C	C	C	C
230	A	A	A	A	A	A	C	C	C	C	C	C
231	A	A	A	A	A	A	C	C	C	C	C	C
232	C	C	C	C	C	C	C	C	C	C	C	C
233	C	C	C	C	C	C	C	C	C	C	C	C
234	C	C	C	C	C	C	C	C	C	C	C	C
235	G	G	G	G	G	G	G	C/G	G	C/G	G	C/G

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	C	N
238	G	G	G	G	G	G	T	C	C	C	A	C/G
239	C	C	C	C	C	C	G	G	G	G	T	N
240	C	C	C	C	C	C	G	G	G	G	C	G
241	G	G	G	G	G	G	A	A	A	A	G	A/T
242	G	G	G	G	G	G	A	A	A	A	G	G
243	A	A	A	A	A	A	A	A	A	A	A	A
244	A	A	A	A	A	A	A	A	A	A	A	A
245	C	C	C	C	C	C	A	C	A	A	A	A
246	A	A	A	A	A	A	G	R	R	R	T	N
247	C	C	C	C	C	C	T	Y	Y	Y	T	N
248	C	C	C	C	C	C	G	C	C	C	T	N
249	C	C	C	C	C	C	T	C	C	C	T	N
250	A	A	A	A	A	A	G	R	R	R	C	N
251	A	A	A	A	A	A	T	N	N	N	A	A/T
252	T	T	T	T	T	T	G	G	G	G	A	G/C
253	G	G	G	G	G	G	T	C	C	C	T	Y
254	T	T	T	T	T	T	C	G	G	G	G	G/C
255	G	G	G	G	G	G	A	A	A	A	A	G
256	A	A	A	A	A	A	C	C	C	C	C	G/C
257	A	A	A	A	A	A	G	G	G	G	C	N
258	G	G	G	G	G	G	T	T	T	T	C	N
259	T	T	T	T	T	T	G	R	R	R	A	N
260	C	C	C	C	C	C	T	Y	Y	Y	C	N
261	C	C	C	C	C	C	T	T	T	T	T	N
262	T	T	T	T	T	T	G	C	C	C	T	A
263	C	C	C	C	C	C	A	R	R	R	A	R
264	A	A	A	A	A	A	G	R	R	R	G	R
265	A	A	A	A	A	A	G	C	C	C	A	R
266	A	A	A	A	A	A	C	N	N	N	C	R
267	G	G	G	G	G	G	C	C	C	C	G	C/G
268	C	C	C	C	C	C	A	A	A	A	A	A
269	C	C	C	C	C	C	A	A	A	A	A	A
270	A	A	A	A	A	A	A	A	A	A	A	A
271	A	A	A	A	A	A	A	A	A	A	A	A
272	G	G	G	G	G	G	G	G	G	G	A	R
273	C	C	C	C	C	C	G	C	C	C	T	N
274	T	T	T	T	T	T	G	T	T	T	T	C
275	G	G	G	G	G	G	A	R	R	R	A	N
276	A	A	A	A	A	A	G	N	N	N	G	N
277	A	A	A	A	A	A	A	A	A	A	A	R
278	G	G	G	G	G	G	G	N	N	N	C	N
279	C	C	C	C	C	C	A	A	A	A	A	R
280	A	A	A	A	A	A	G	N	N	N	A	N
281	T	T	T	T	T	T	T	T	T	T	C	N
282	C	C	C	C	C	C	G	C	C	C	T	N
283	G	G	G	G	G	G	C	C	C	C	C	N
284	T	T	T	T	T	T	A	A	A	A	T	N
285	G	G	G	G	G	G	T	T	T	T	G	N
286	G	G	G	G	G	G	C	C	C	C	C	N
287	C	C	C	C	C	C	T	T	T	T	T	N
288	A	A	A	A	A	A	G	G	G	G	A	N
289	G	G	G	G	G	G	C	C	C	C	G	C/G
290	C	C	C	C	C	C	A	A	A	A	A	R
291							C	C	C	C	G	N
292							A	A	A	A	A	A/T
293							C	C	C	C	T	N
294							G	G	G	G	C	N
295	G	G	G	G	G	G	A	A	A	A	T	C
296	A	A	A	A	A	A	C	C	C	C	G	G
297	C	C	C	C	C	C	A	A	A	A	A	R
298	G	G	G	G	G	G	A	A	A	A	A	A
299	A	A	A	A	A	A	A	A	A	A	A	A
300	A	A	A	A	A	A	A	A	A	A	A	A
301	G	G	G	G	G	G	A	A	A	A	A	A
302	A	A	A	A	A	A	R	R	R	R	A	R
303	G	G	G	G	G	G	T	T	T	T	G	R
304	T	T	T	T	T	T	G	G	G	G	T	Y
305	G	G	G	G	G	G	A	A	A	A	N	R
306	A	A	A	A	A	A	C	C	C	C	A	R
307	C	C	C	C	C	C	G	G	G	G	T	N
308	A	A	A	A	A	A	A	A	A	A	A	R
309	A	A	A	A	A	A	A	A	A	A	A	R
310	A	A	A	A	A	A	A	A	A	A	A	R
311	G	G	G	G	G	G	A	A	A	A	C	N
312	A	A	A	A	A	A	T	T	T	T	T	A/T
313	T	T	T	T	T	T	C	C	C	C	T	C/G
314	C	C	C	C	C	C	A	A	A	A	G	N
315	T	T	T	T	T	T	T	T	T	T	T	Y
316	G	G	G	G	G	G	C	C	C	C	T	N
317	T	T	T	T	T	T	G	G	G	G	T	N
318	C	C	C	C	C	C	A	A	A	A	A	N
319	A	A	A	A	A	A	A	A	A	A	C	N
320	G	G	G	G	G	G	T	T	T	T	G	N
321	A	A	A	A	A	A	A	A	A	A	C	N
322	A	A	A	A	A	A	A	A	A	A	A	A
323	A	A	A	A	A	A	G	G	G	G	A	N
324	T	T	T	T	T	T	T	T	T	T	T	N
325	C	C	C	C	C	C	G	G	G	G	G	G/C
326	G	G	G	G	G	G	C	C	C	C	T	N
327	T	T	T	T	T	T	G	G	G	G	C	G/C
328	G	G	G	G	G	G	T	T	T	T	G	N
329	G	G	G	G	G	G	C	C	C	C	C	G/C
330	T	T	T	T	T	T	A	A	A	A	A	N
331	C	C	C	C	C	C	T	T	T	T	T	N
332	A	A	A	A	A	A	A	A	A	A	A	N
333	A	A	A	A	A	A	A	A	A	A	A	N
334	A	A	A	A	A	A	A	A	A	A	A	N
335	G	G	G	G	G	G	A	A	A	A	A	N
336	A	A	A	A	A	A	G	G	G	G	A	G
337	A	A	A	A	A	A	A	A	A	A	A	A
338	G	G	G	G	G	G	A	A	A	A	A	R
339	C	C	C	C	C	C	G	G	G	G	A	N
340	C	C	C	C	C	C	A	A	A	A	A	N
341	C	C	C	C	C	C	T	T	T	T	C	N
342	A	A	A	A	A	A	C	C	C	C	A	N
343	C	C	C	C	C	C	A	A	A	A	C	N
344	C	C	C	C	C	C	A	A	A	A	T	Y
345	A	A	A	A	A	A	T	T	T	T	C	N
346	C	C	C	C	C	C	G	G	G	G	C	C/G
347	C	C	C	C	C	C	T	T	T	T	C	N
348	A	A	A	A	A	A	A	A	A	A	T	N
349	G	G	G	G	G	G	A	A	A	A	C	N
350	A	A	A	A	A	A	A	A	A	A	A	R
351	G	G	G	G	G	G	A	A	A	A	A	N
352	A	A	A	A	A	A	A	A	A	A	A	N
353							A	A	A	A	A	A/T

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	A	C	N	T	N
356	C	C	C	C	C	C	C	C	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	G	G/C	T	N
358	G	G	G	G	G	G	G	G	C	N	C	N
359	C	C	C	C	C	C	T	C	A	N	A	N
360	T	T	T	T	T	T	T	T	T	N	G	N
361	T	T	T	T	T	T	T	T	T	T	C	N
362	A	A	A	A	A	A	A	A	A	A	A	N
363	T	T	T	T	T	T	T	T	T	T	G	N
364	G	G	G	G	G	G	A	A	A	R	C	R
365	A	A	A	A	A	A	A	A	G	A	A	A
366	A	A	A	A	A	A	T	A	T	N	C	N
367	C	C	C	C	C	C	C	C	T	A	A	N
368	C	C	C	C	C	C	T	T	A	N	T	A
369	T	T	T	T	T	T	T	T	C	Y	T	Y
370	T	T	T	T	T	T	T	T	A	N	T	Y
371	T	T	T	T	T	T	T	T	C	Y	T	Y
372	C	C	C	C	C	C	A	A	A	N	T	A
373	A	A	A	A	A	A	A	A	A	A	A	A
374	A	A	A	A	A	A	A	A	A	N	A	A
375	G	G	G	G	G	G	T	T	G	N	T	N
376	T	T	T	T	T	T	T	T	T	N	G	N
377	G	G	G	G	G	G	T	T	T	N	T	N
378	T	T	T	T	T	T	C	C	A	N	G	N
379	A	A	A	A	A	A	T	T	A	T/A	T	T/A
380	T	T	T	T	T	T	C	C	T	Y	T	Y
381	T	T	T	T	T	T	A	A	T	T/A	C	N
382	T	T	T	T	T	T	T	T	T	A	T	N
383	A	A	A	A	A	A	T	T	G	N	C	N
384	C	C	C	C	C	C	G	G	A	N	A	N
385	G	G	G	G	G	G	A	A	G	R	C	R
386	A	A	A	A	A	A	A	A	G	N	A	A
387	C	C	C	C	C	C	A	A	A	N	A	N
388	A	A	A	A	A	A	A	A	C	A	C	N
389	G	G	G	G	G	G	A	A	A	R	G	R
390	C	C	C	C	C	C	C	C	G	N	T	N
391	A	A	A	A	A	A	A	A	A	A	A	A
392	A	A	A	A	A	A	A	A	A	R	A	R
393	A	A	A	A	A	A	A	A	A	N	G	N
394	C	C	C	C	C	C	C	C	C	C	C	C
395	T	T	T	T	T	T	A	A	A	T/A	G	N
396	T	T	T	T	T	T	A	A	A	T/A	C	N
397	G	G	G	G	G	G	A	A	A	R	T	T
398	A	A	A	A	A	A	G	G	T	N	T	N
399	T	T	T	T	T	T	T	T	T	A	T	A
400	T	T	T	T	T	T	T	T	T	N	T	N
401	T	T	T	T	T	T	T	T	T	Y	Y	Y
402	T	T	T	T	T	T	T	T	T	Y	Y	Y
403	C	C	C	C	C	C	C	C	C	N	C	N
404	T	T	T	T	T	T	C	C	T/A	N	T	N
405	C	C	C	C	C	C	C	C	C	N	C	N
406	T	T	T	T	T	T	A	A	T/A	R	Y	R
407	A	A	A	A	A	A	T	T	A	T	T	T
408	T	T	T	T	T	T	G	G	T	A	T	A
409	T	T	T	T	T	T	A	A	T	T	T	T
410	A	A	A	A	A	A	T	T	A	T	T	T
411	T	T	T	T	T	T	G	G	T	T	T	T
412	G	G	G	G	G	G	A	A	T	T	T	T
413	A	A	A	A	A	A	T	T	T	T	T	T
414	T	T	T	T	T	T	A	A	T	T	T	T
415	T	T	T	T	T	T	T	T	T	T	T	T
416	T	T	T	T	T	T	T	T	T	T	T	T
417	A	A	A	A	A	A	T	T	T	T	T	T
418	T	T	T	T	T	T	A	A	T	T	T	T
419	T	T	T	T	T	T	A	A	T	T	T	T
420	T	T	T	T	T	T	T	T	T	T	T	T
421	G	G	G	G	G	G	C	C	C	Y	G	N
422	T	T	T	T	T	T	C	C	A	G/C	G	N
423	T	T	T	T	T	T	A	A	C	T/A	T	N
424	T	T	T	T	T	T	T	T	C	Y	T	N
425	T	T	T	T	T	T	T	T	C	N	C	N
426	T	T	T	T	T	T	T	T	C	N	T	N
427	G	G	G	G	G	G	G	G	T	A	C	N
428	T	T	T	T	T	T	A	A	T	Y	T	N
429	A	A	A	A	A	A	T	T	T	N	T	N
430	T	T	T	T	T	T	T	T	T	N	C	N
431	T	T	T	T	T	T	T	T	T	T/A	G	T/A
432	T	T	T	T	T	T	G	G	T	N	A	N
433	G	G	G	G	G	G	A	A	T	N	A	N
434	C	C	C	C	C	C	T	T	A	N	C	N
435	T	T	T	T	T	T	A	A	T	R	T	A
436	G	G	G	G	G	G	A	A	A	A	T	N
437	A	A	A	A	A	A	T	T	A	A	T	N
438	A	A	A	A	A	A	G	G	A	A	T	N
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443	T	T	T	T	T	T	T	T	T	T	T	N
444	G	G	G	G	G	G	A	A	A	T	T	N
445	A	A	A	A	A	A	A	A	A	A	T	N
446	C	C	C	C	C	C	A	A	A	A	T	N
447	T	T	T	T	T	T	T	T	T	T	T	N
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449	T	T	T	T	T	T	T	T	T	T	T	N
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469	T	T	T	T	T	T	T	T	T	T	T	N
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471	T	T	T	T	T	T	T	T	T	T	T	N

Fig. 7.2 cont.

202210 01152366

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
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473	A	T	A	A	A	T	A	A		T	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	T	N
479	G	G	G	G	G	G	T	N		N	T	N
480	T	T	T	T	T	T	G	N		N	T	N
481	A	A	A	A	A	A	T	N		N	A	N
482	A	C	C	C	C	C	T	Y		Y	A	N
483	T	T	T	T	T	T	T	T		T	A	AT
484	A	A	A	A	A	A	C	N		N	G	N
485	T	T	T	T	T	T	T	T		T	A	AT
486	C	C	C	C	C	C	G	N		N	A	N
487	G	G	G	G	G	G	A	R		R	A	R
488	T	T	T	T	T	T	T	T		T	A	TIA
489	T	T	T	T	T	T	G	N		N	A	N
490	A	A	A	A	A	A	T	N		N	A	N
491	T	T	T	T	T	T	A	N		N	A	R
492	G	A	G	G	G	G	A	R		R	A	N
493	T	A	T	A	T	N	A	N		N	A	N
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
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501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
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512												

Fig. 7.2 cont.

[illegible]

Fig. 7.3

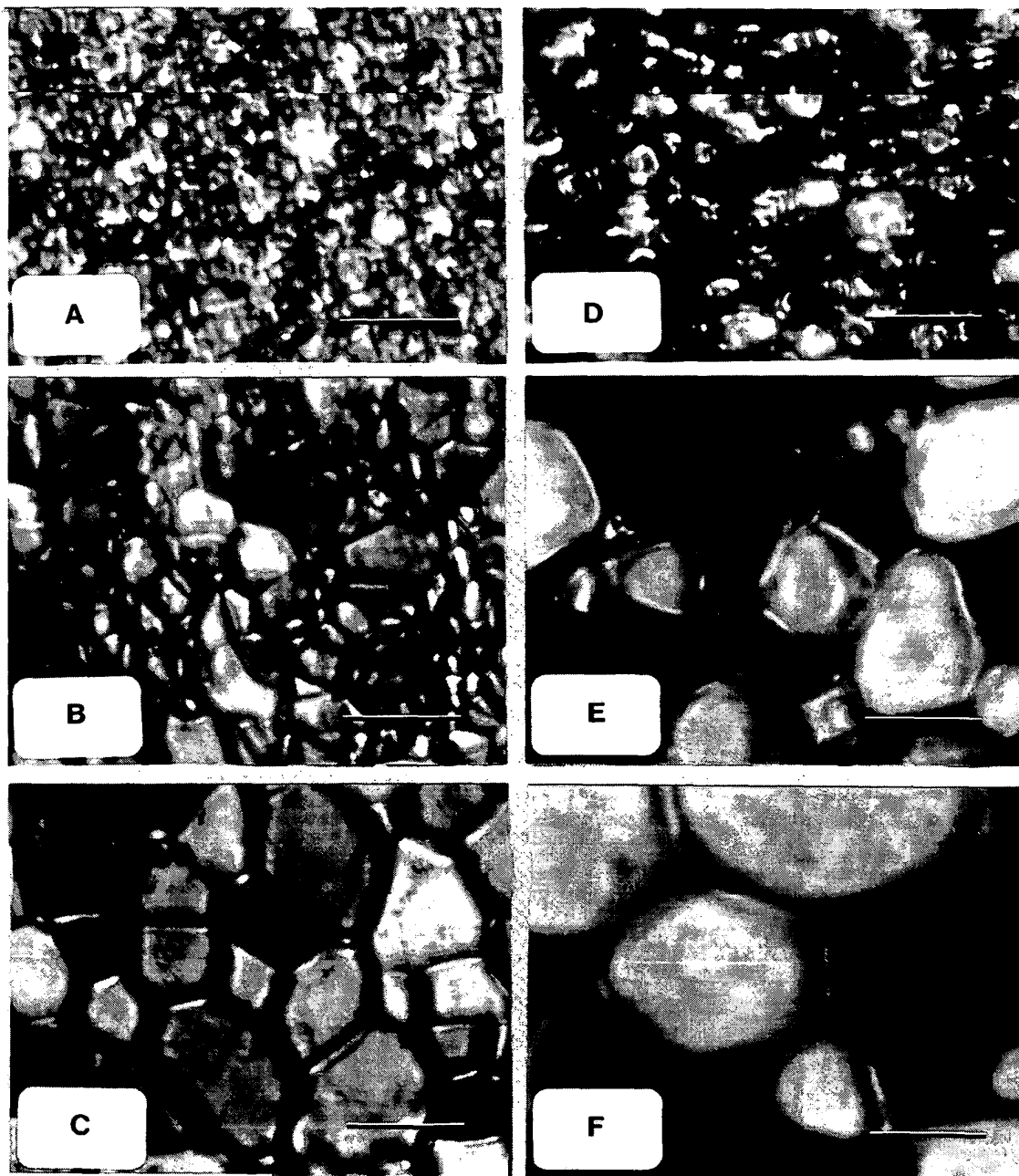


Fig. 8.0

09876349.012802

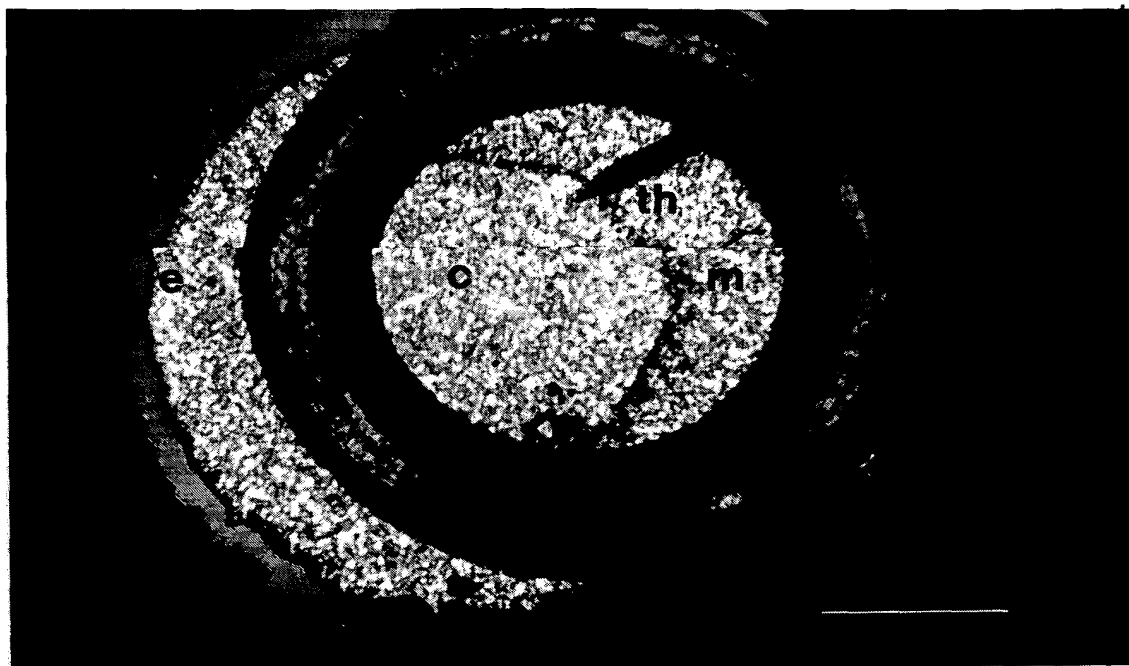


Fig. 8.1a

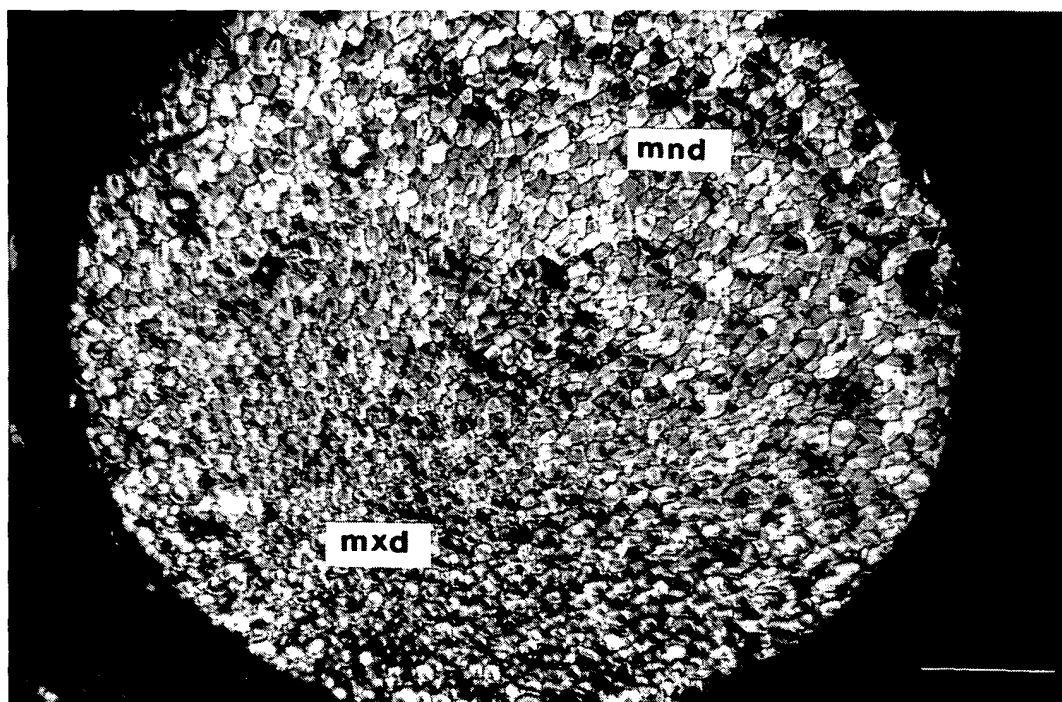
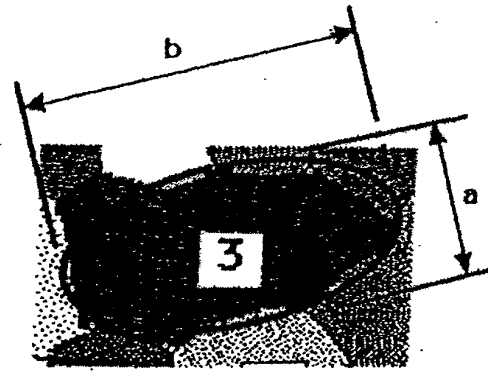
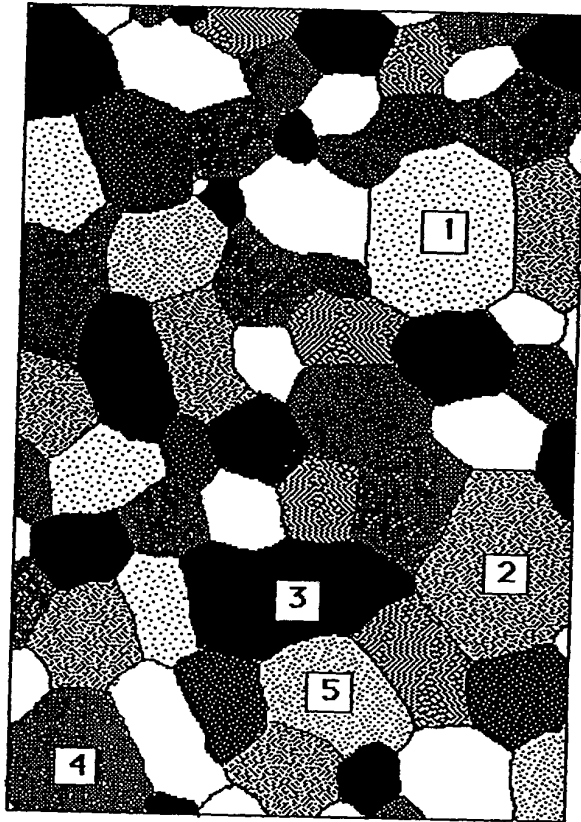


Fig. 8.1b

202210-84E9/860



grain area = $0.25ab$

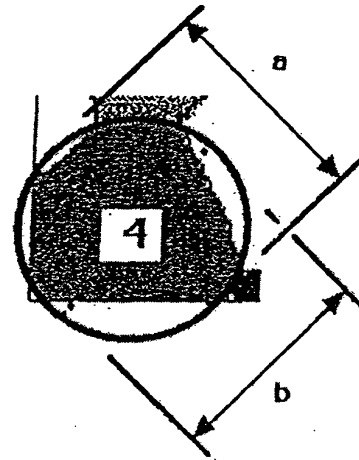


Fig. 8.2

203210" 84E92060

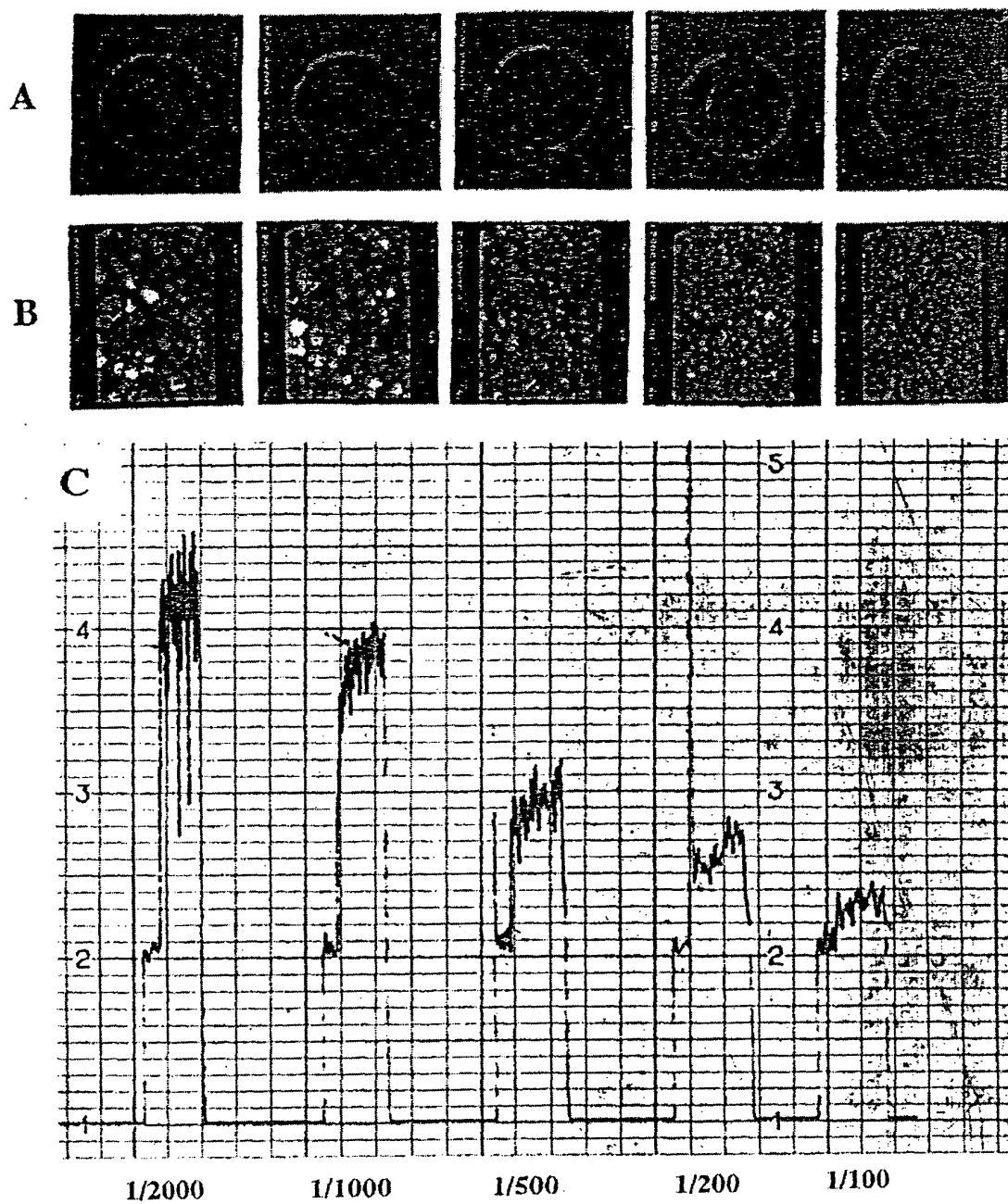


Fig. 8.3

2025-01-09 09:24:00

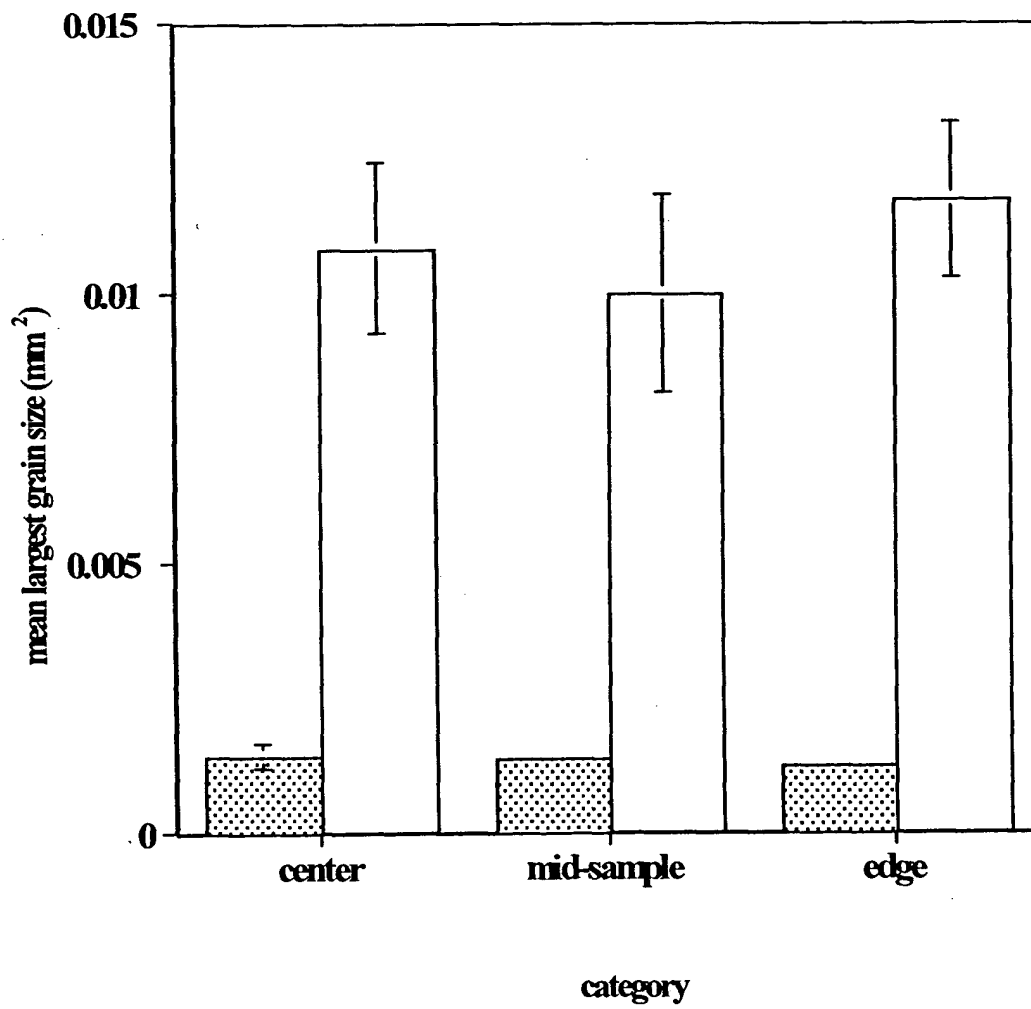


Fig. 8.4a

The figure consists of two electron micrographs, labeled A and B, showing cross-sections of a biological specimen. Image A (top) shows a cell with a large, irregularly shaped vacuole and a prominent nucleus. Image B (bottom) shows a similar cell, but the vacuole is smaller and more rounded. Both images are labeled with 'A' and 'B' in the bottom right corner.

Fig. 8.4b

200210 81E9/860

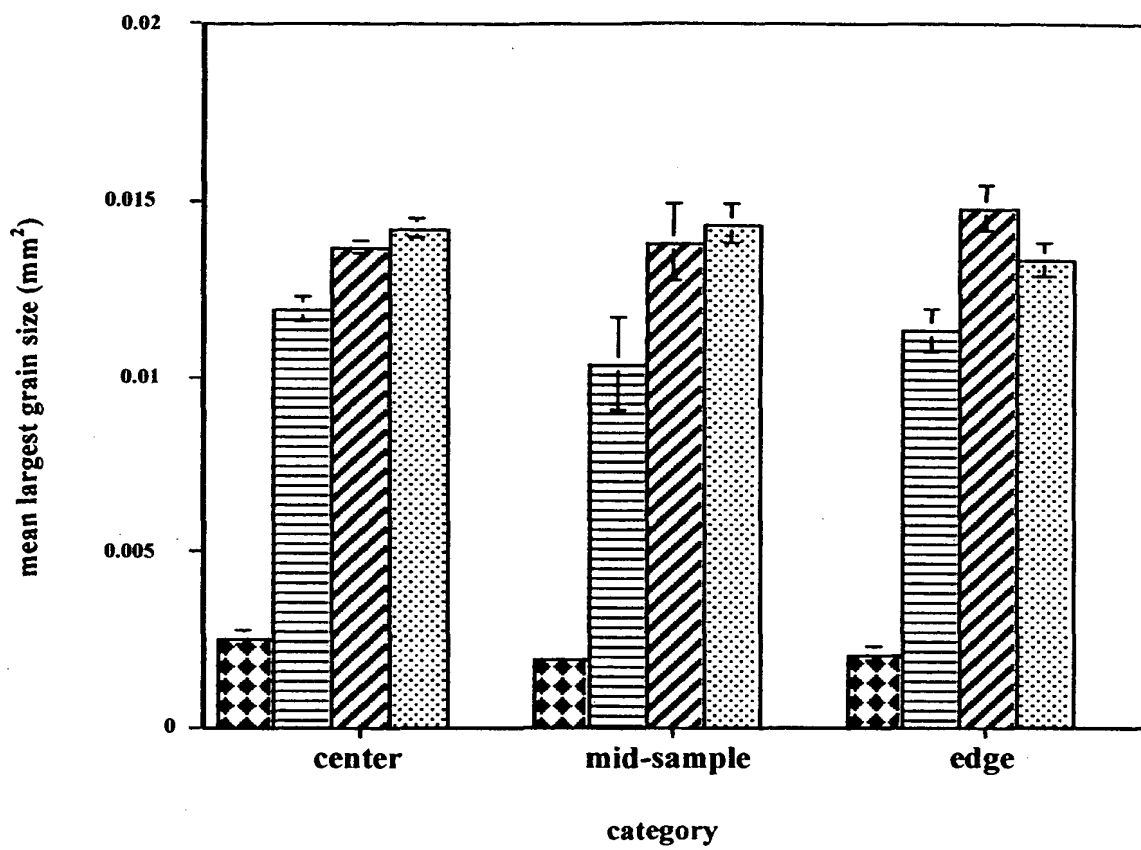


Fig. 8.5a

203210" BH59/860

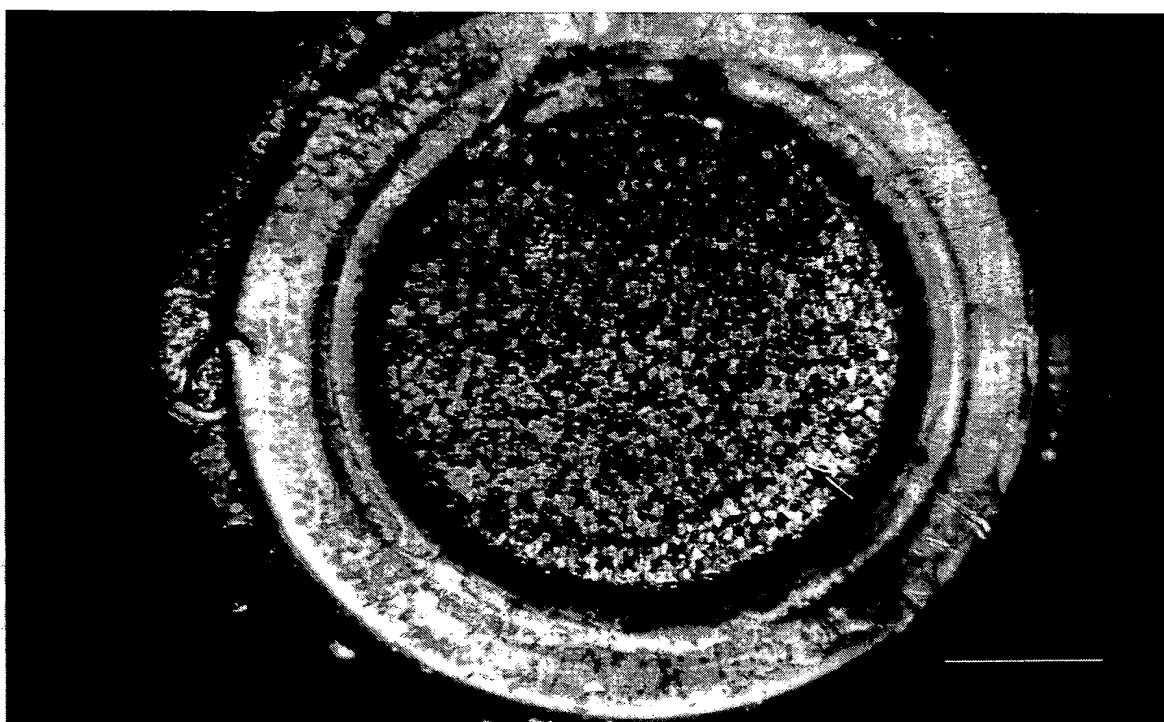


Fig. 8.5b

09875340 012802
200210 04E9/860

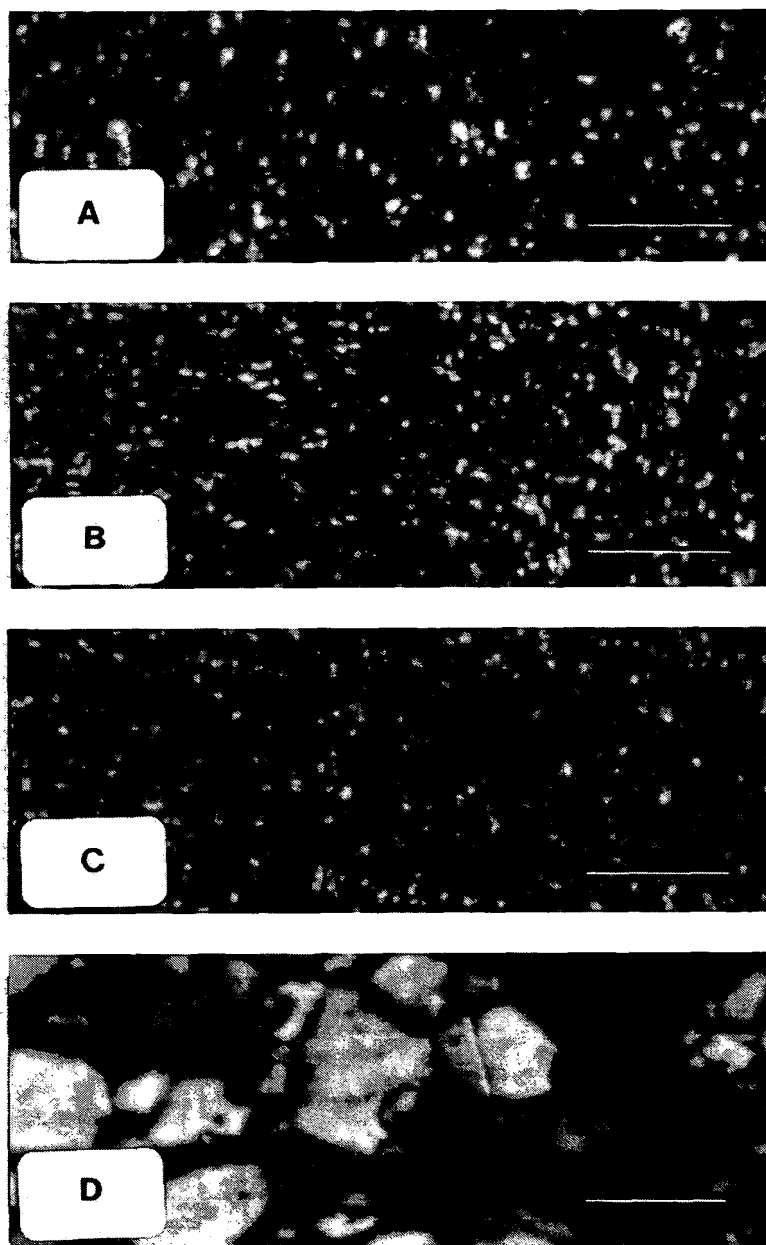


Fig. 8.6

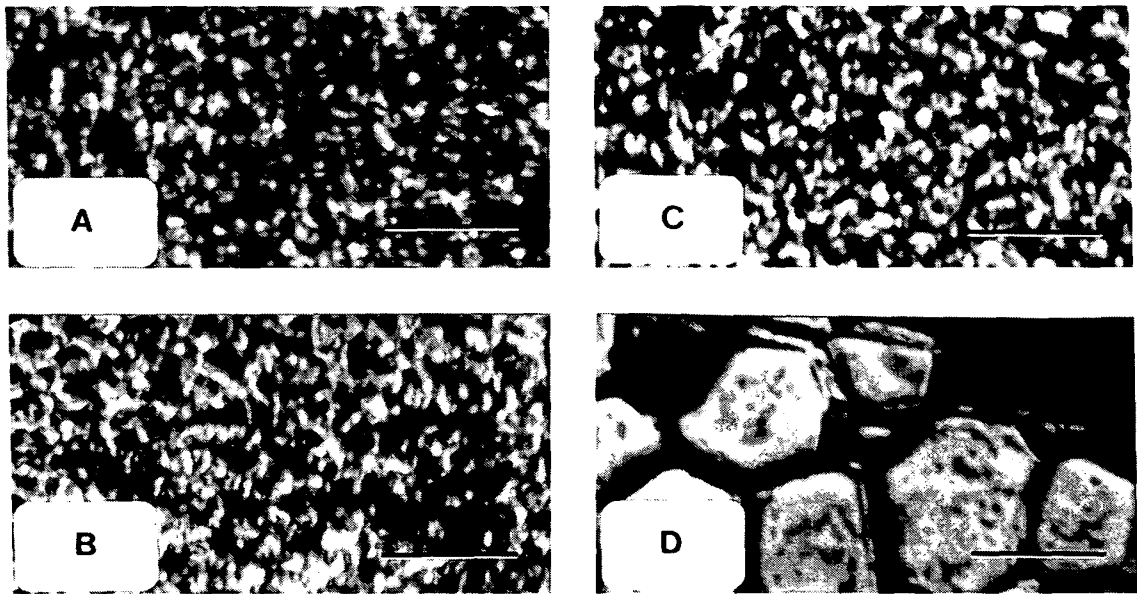


Fig. 8.7

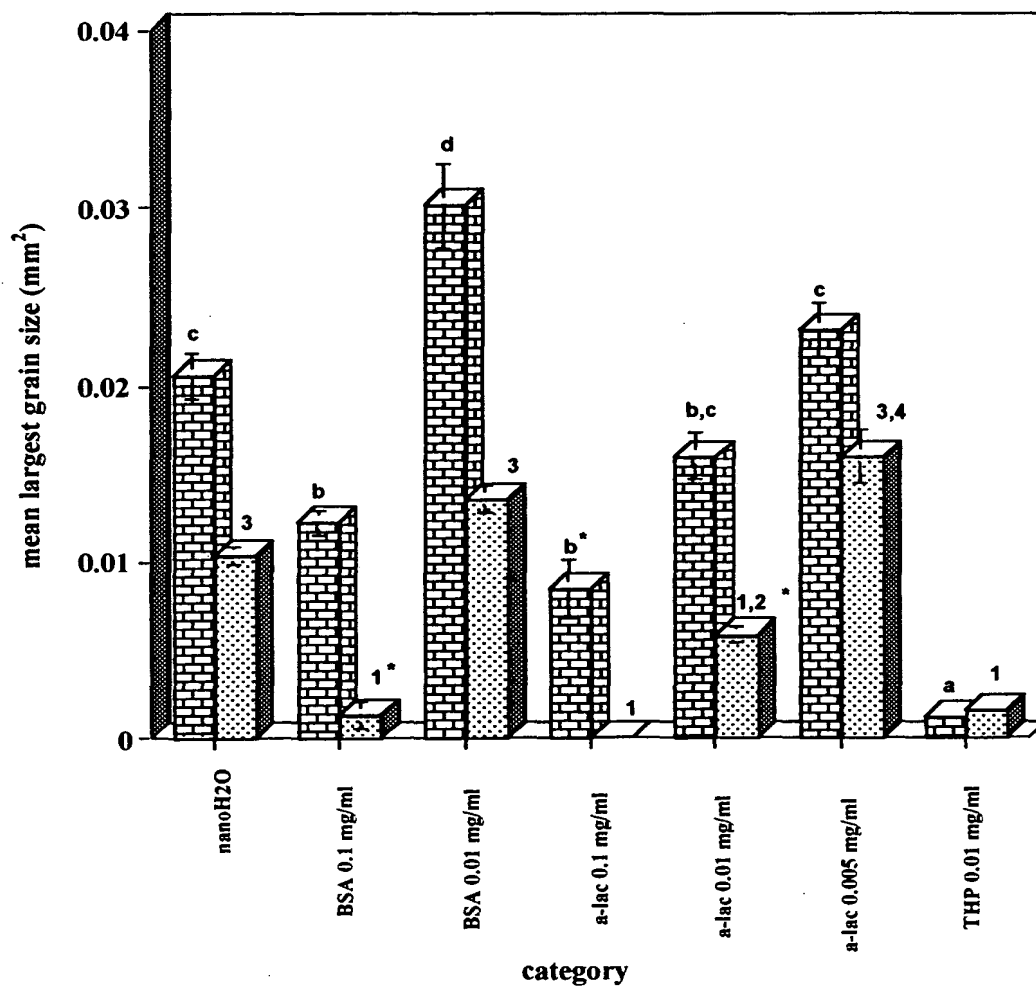


Fig. 8.8

208210" 04E34860

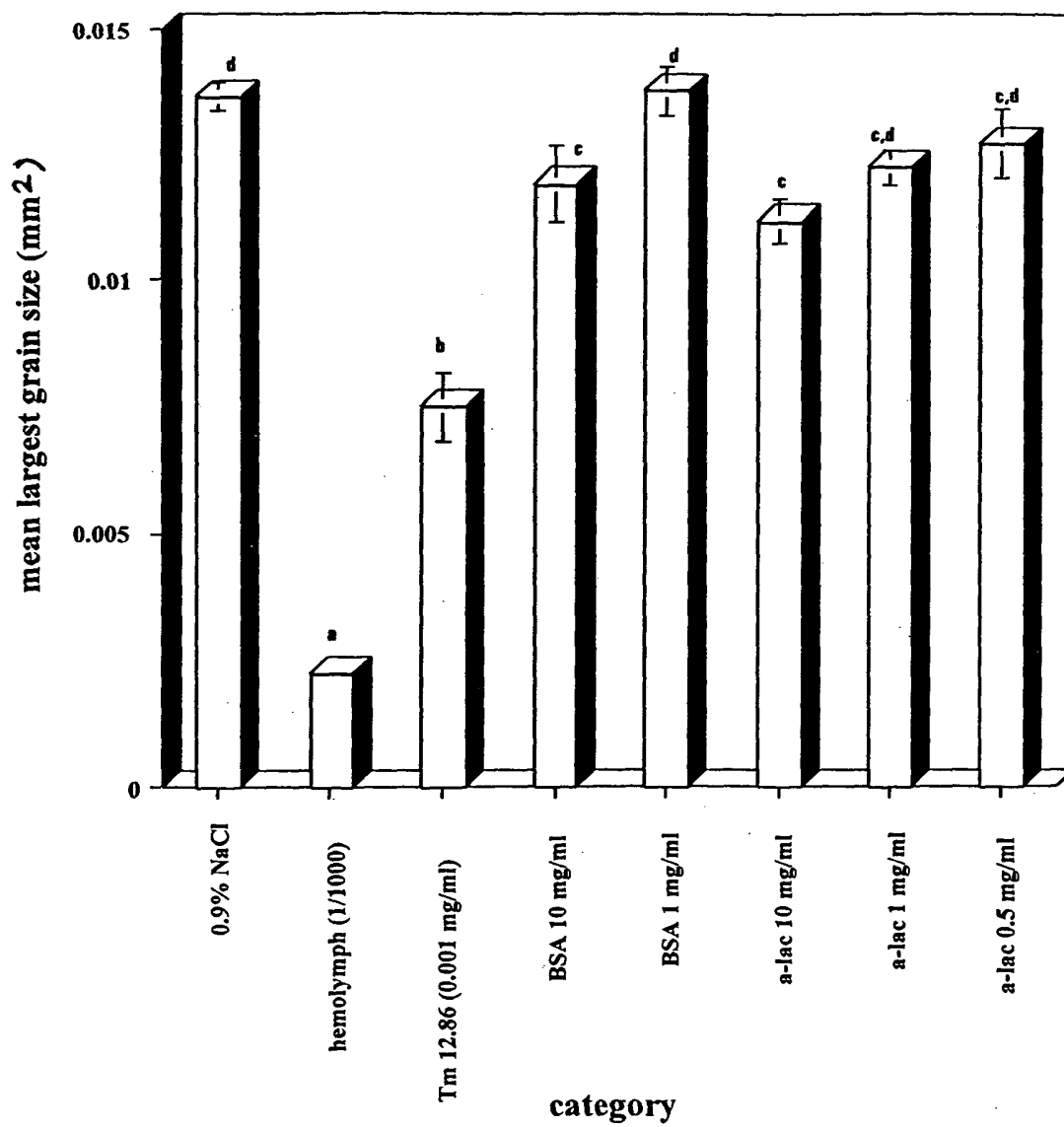


Fig. 8.9

2025-03-28

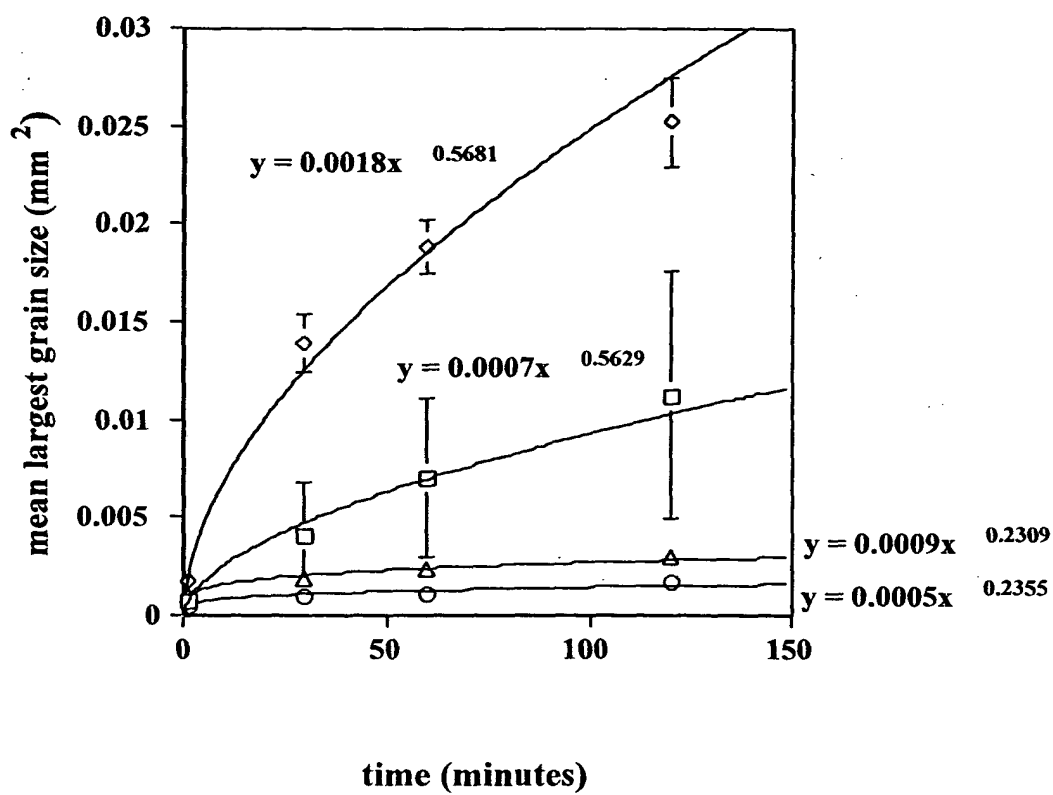


Fig. 8.10

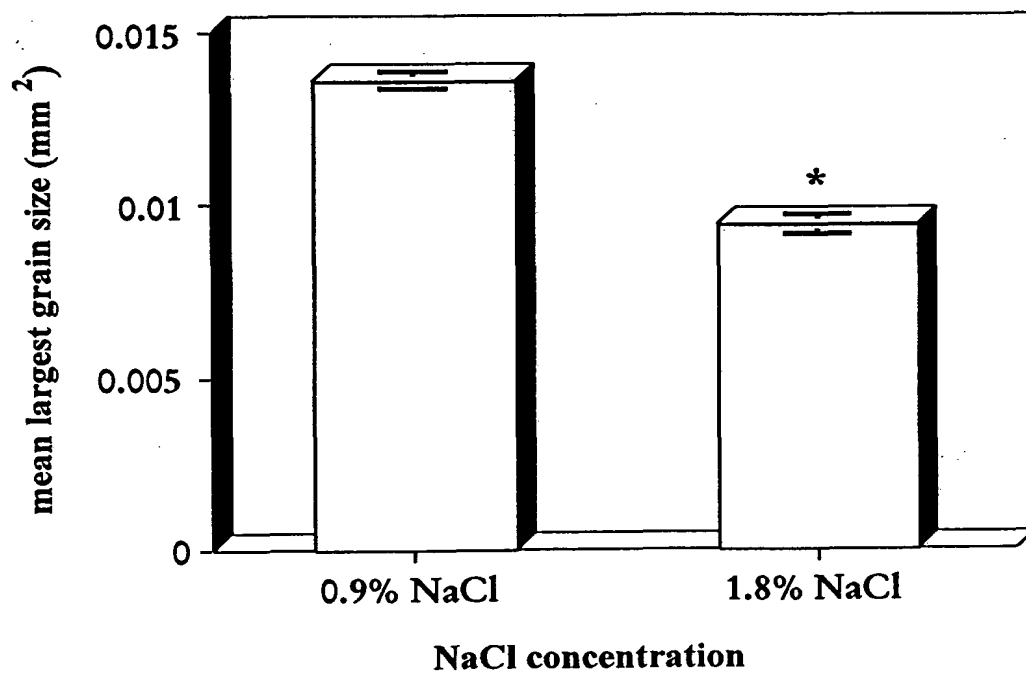
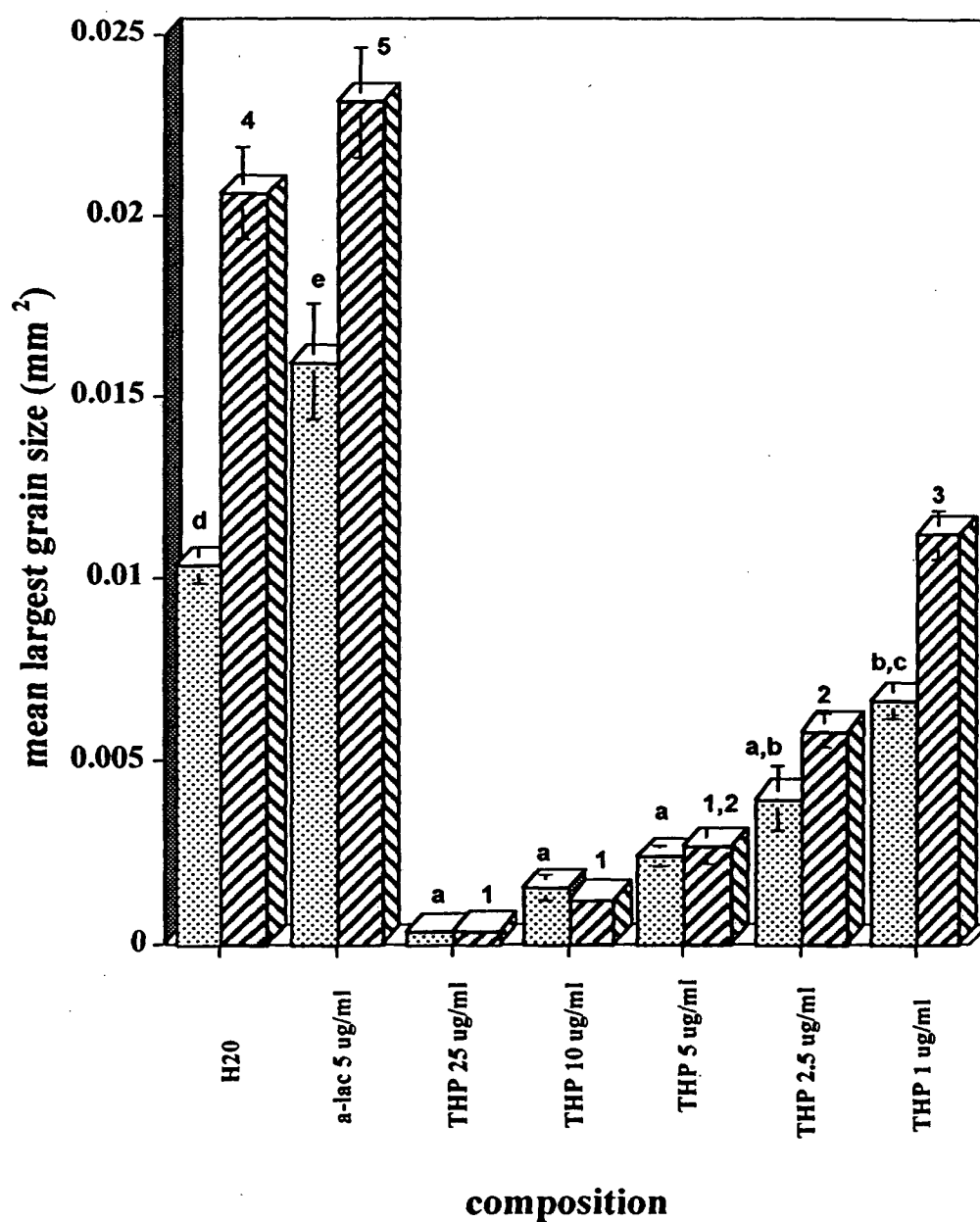


Fig. 8.11

Figure 1 consists of six panels, A through F, showing electron micrographs of the developing chick retina. Panels A through E are arranged vertically on the left, showing a progression of retinal development from 10 to 18 days post-hatching. Panel A (10 days) shows a relatively simple structure with a prominent inner plexiform layer. Panel B (12 days) shows more complex branching in the inner plexiform layer. Panel C (14 days) shows further development of the inner plexiform layer and the beginning of the outer plexiform layer. Panel D (16 days) shows a more developed outer plexiform layer. Panel E (18 days) shows a well-developed outer plexiform layer. Panel F (18 days) is a higher magnification view of the outer plexiform layer, showing the detailed structure of the photoreceptor terminals and the inner plexiform layer. Each panel includes a scale bar in the bottom right corner.

Fig. 8.12

*Fig. 8.13*

200270 0152860

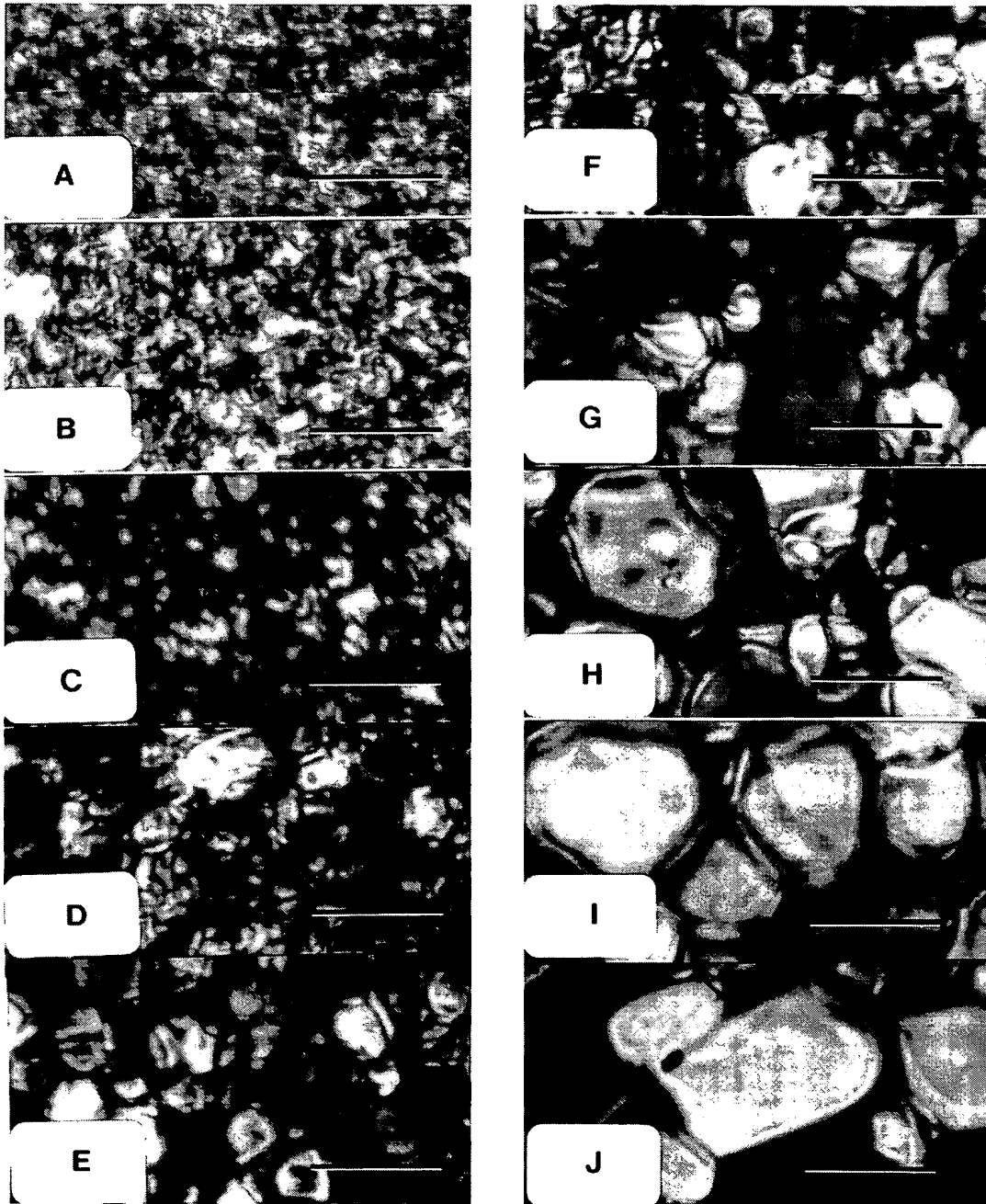


Fig. 8.14

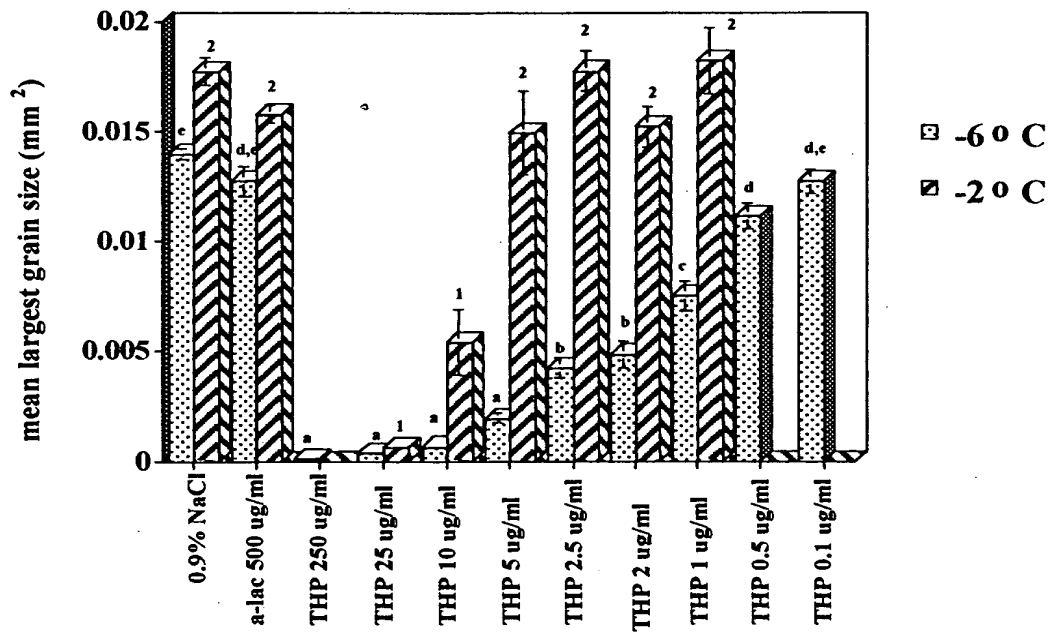


Fig. 8.15

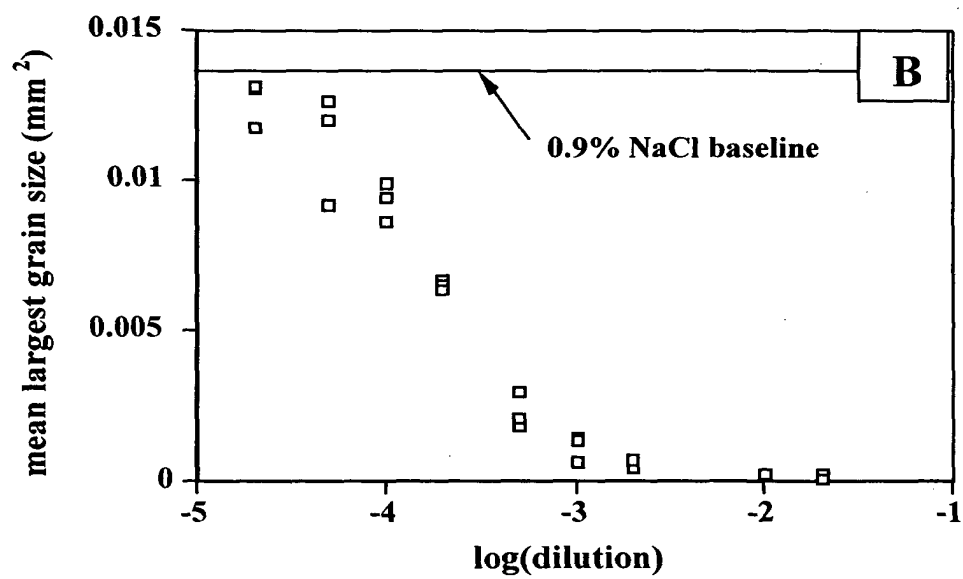
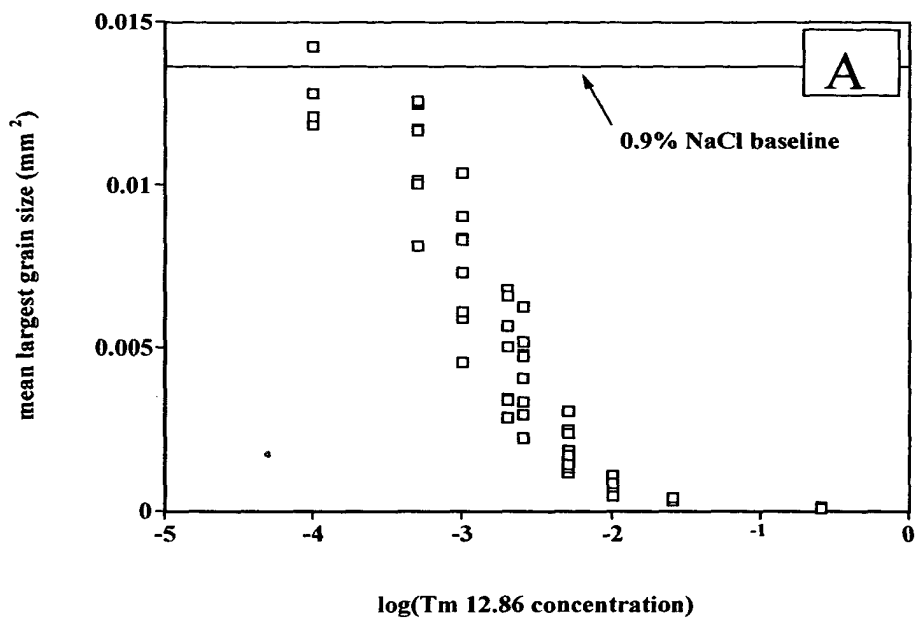


Fig. 8.16

2025-01-27 14:28:10

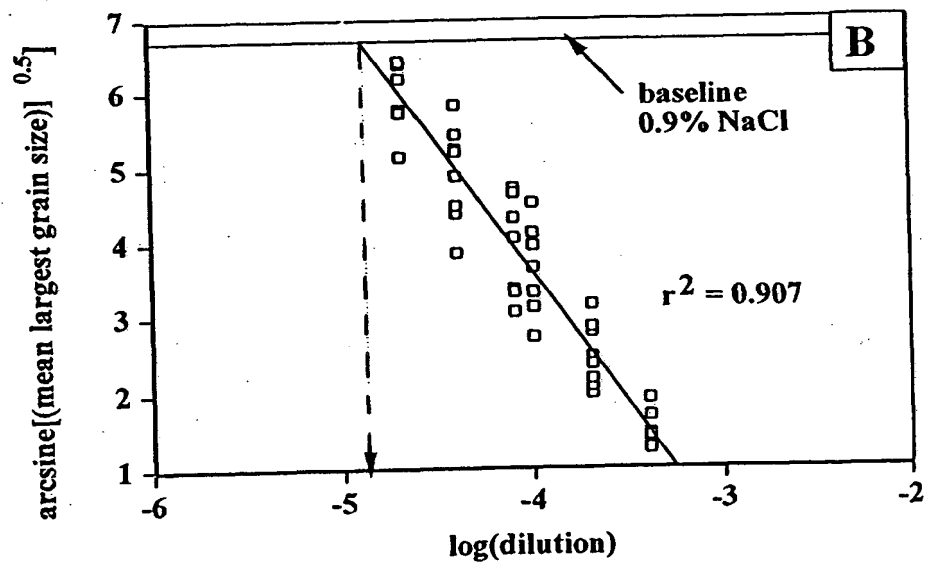
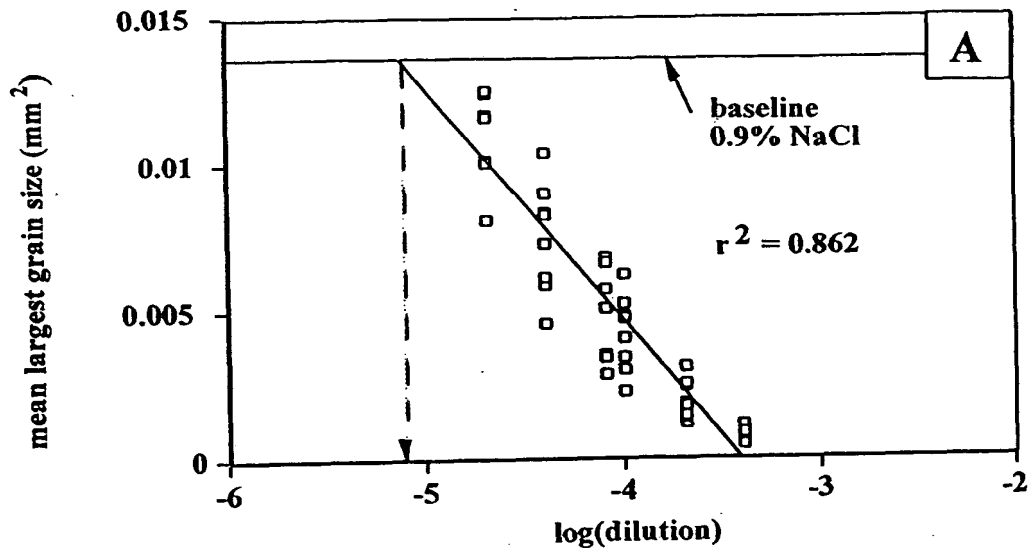


Fig. 8.17

20250707 09:22:00

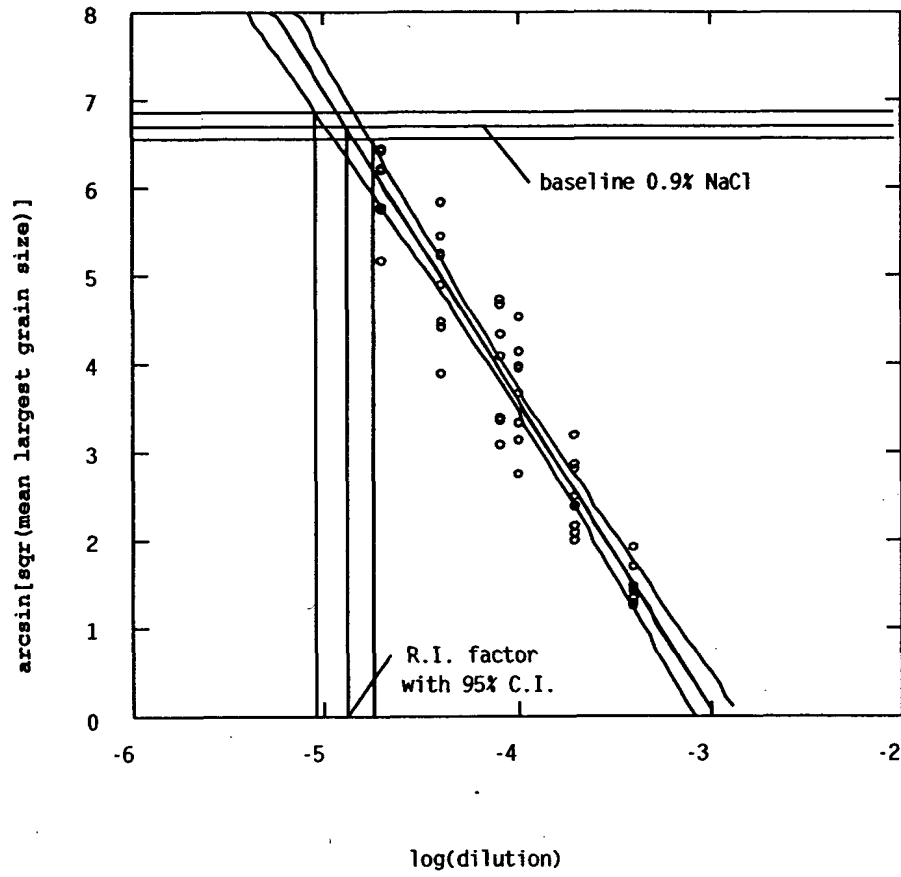


Fig. 8.18

202510 01492860

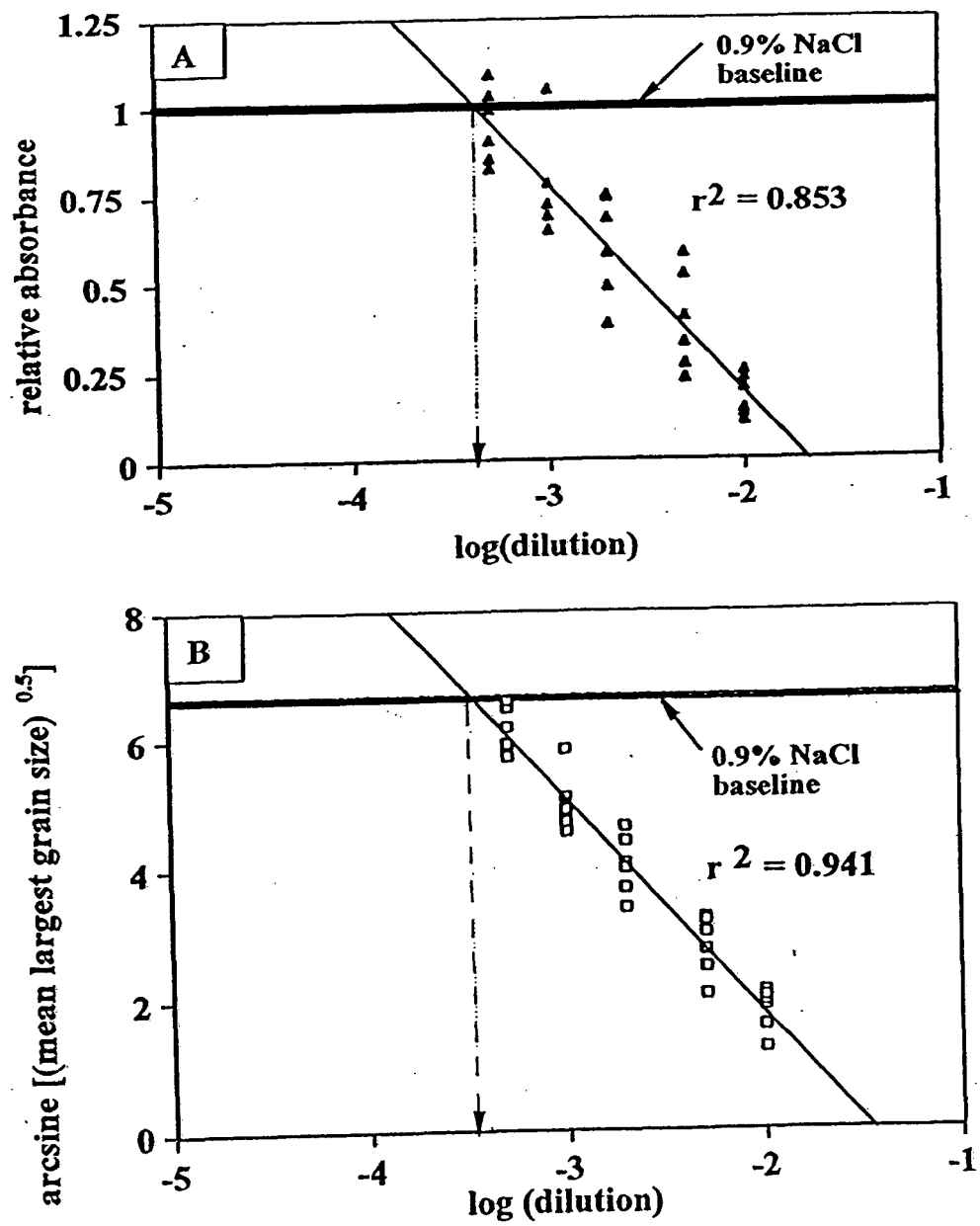


Fig. 8.19

20250709 09:28:00

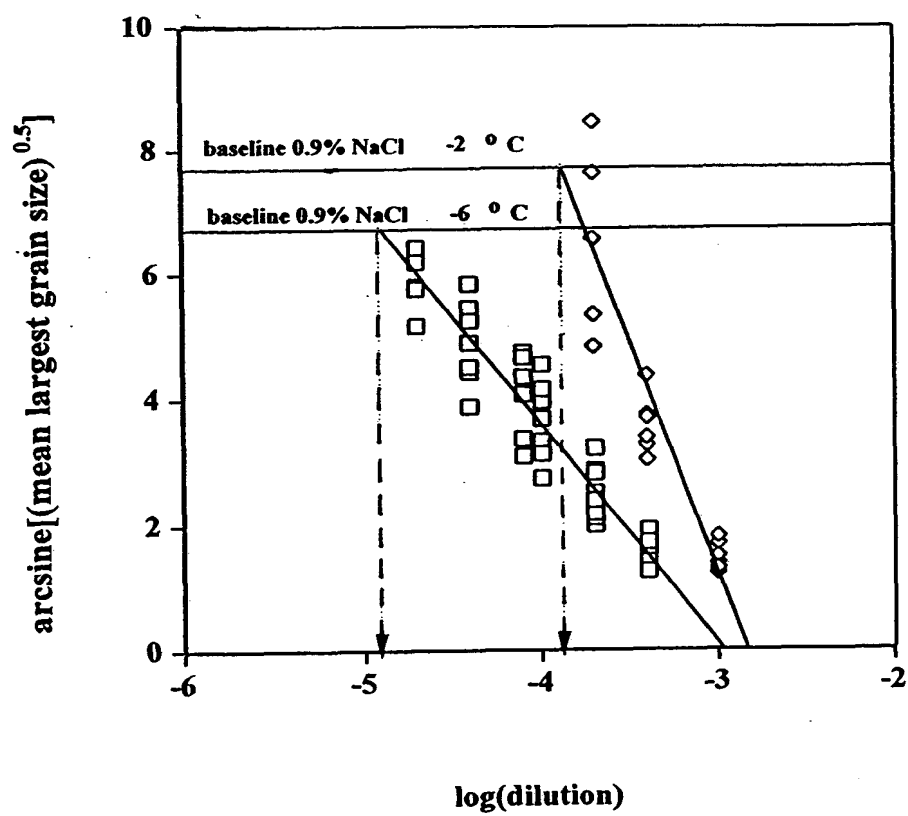


Fig. 8.20

20250101 09:29:00

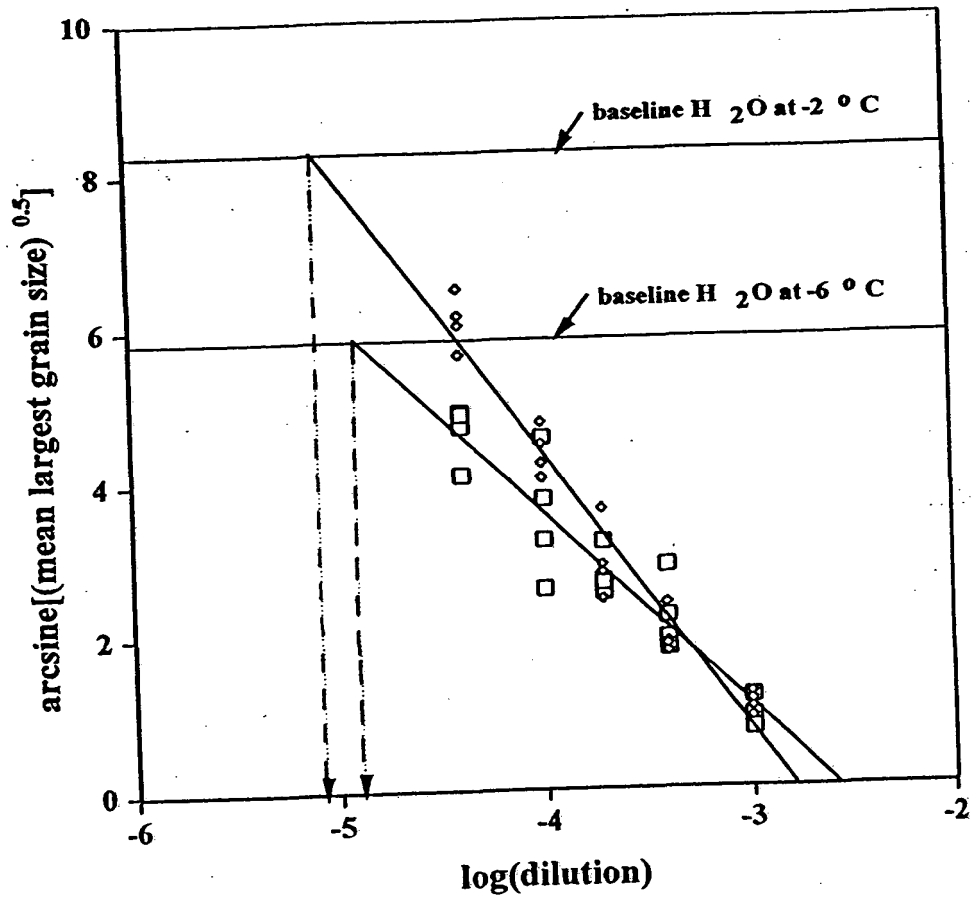


Fig. 8.21

202210 01:52:50

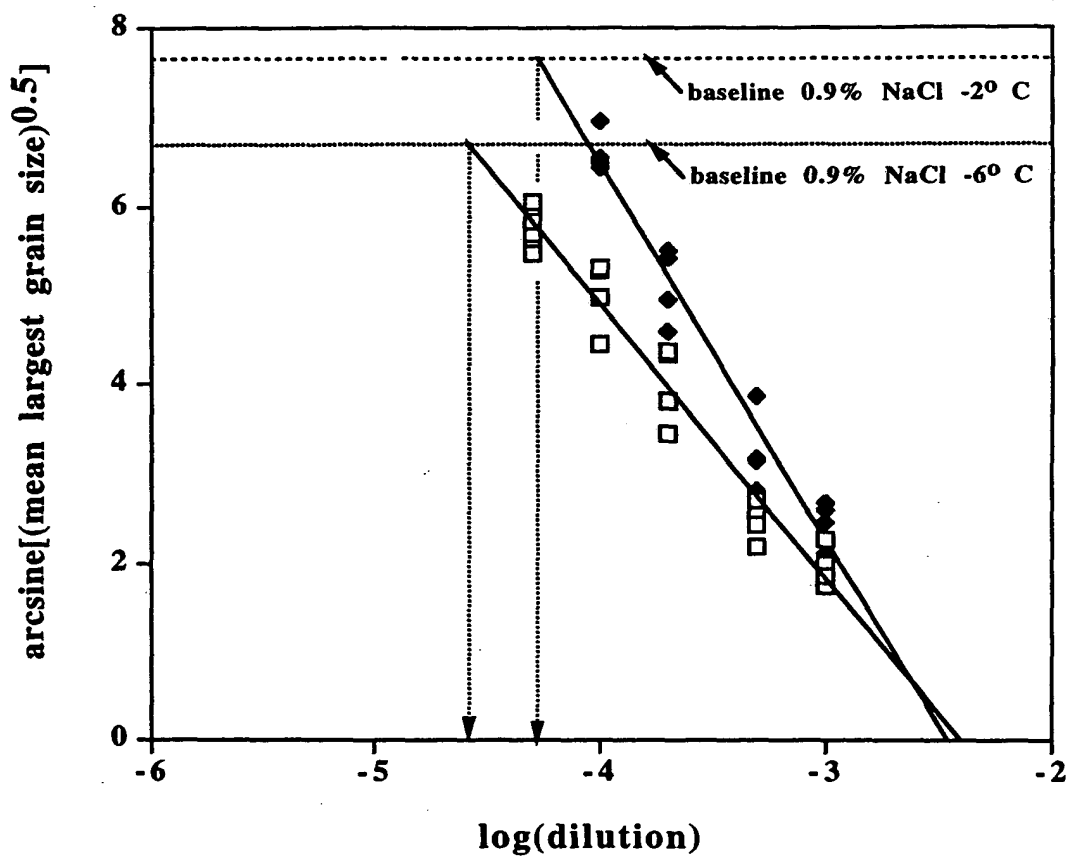


Fig. 8.22

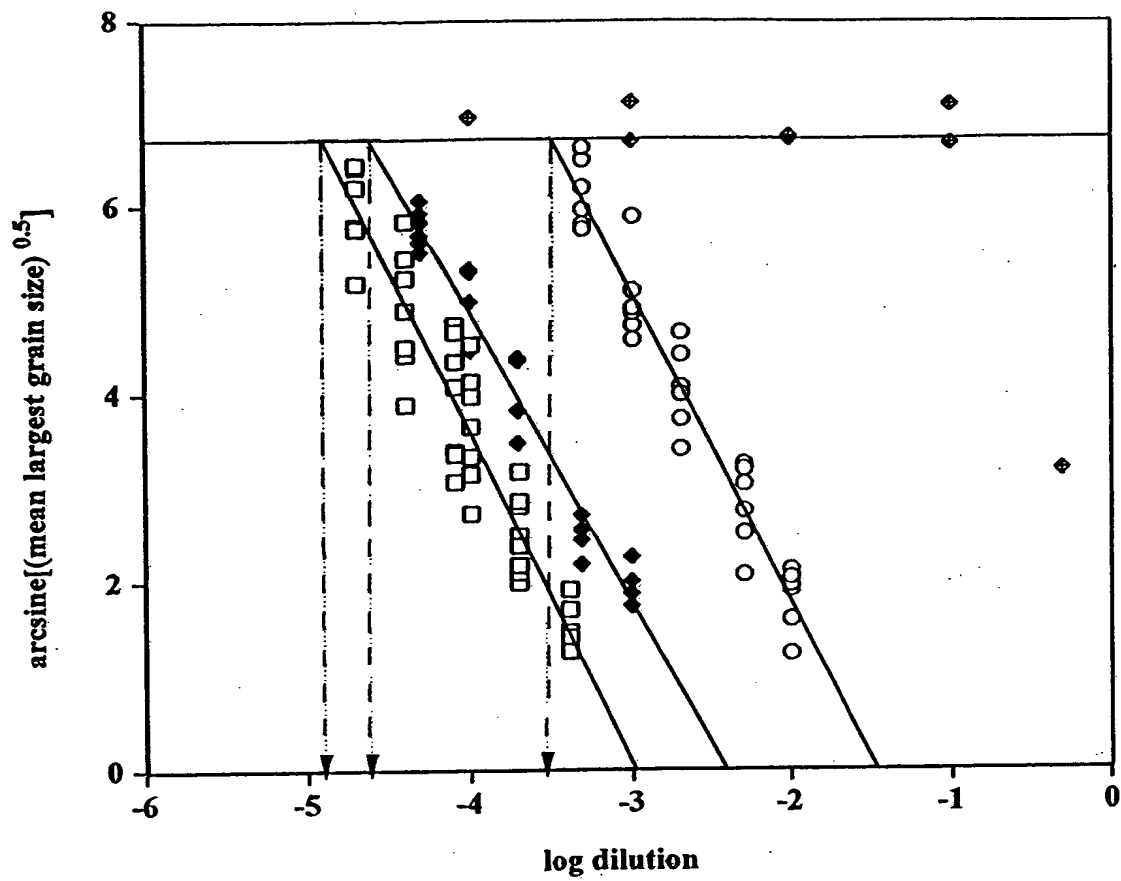


Fig. 8.23

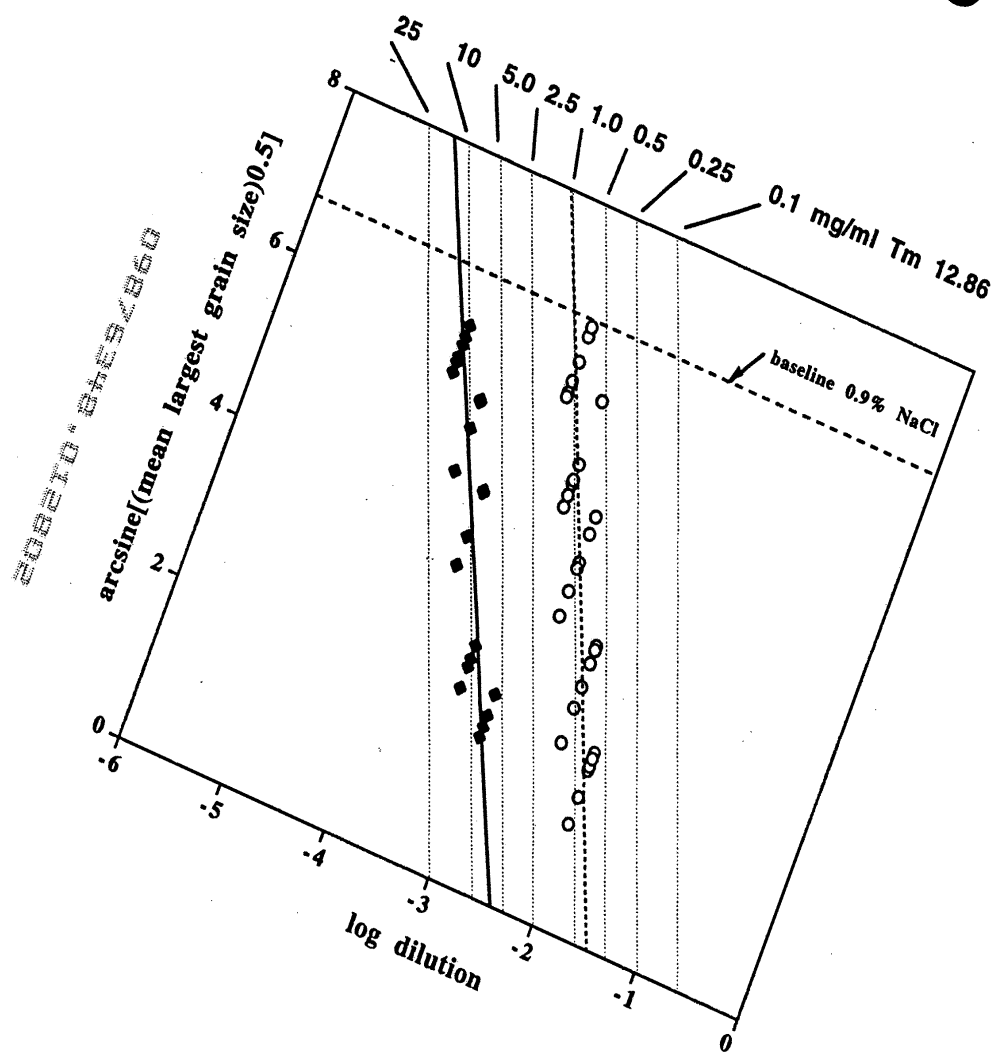


Fig. 8.24

20020701 01:53:25.00

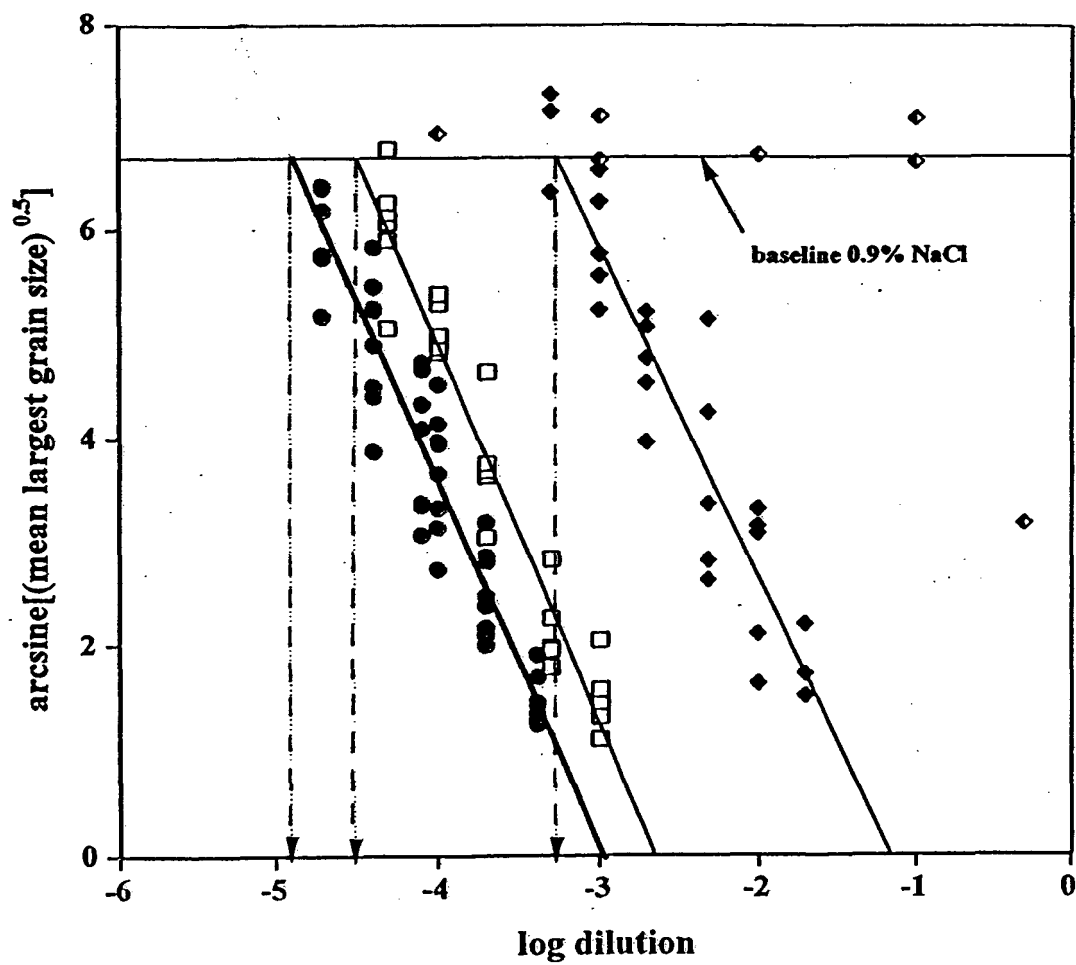


Fig. 8.25

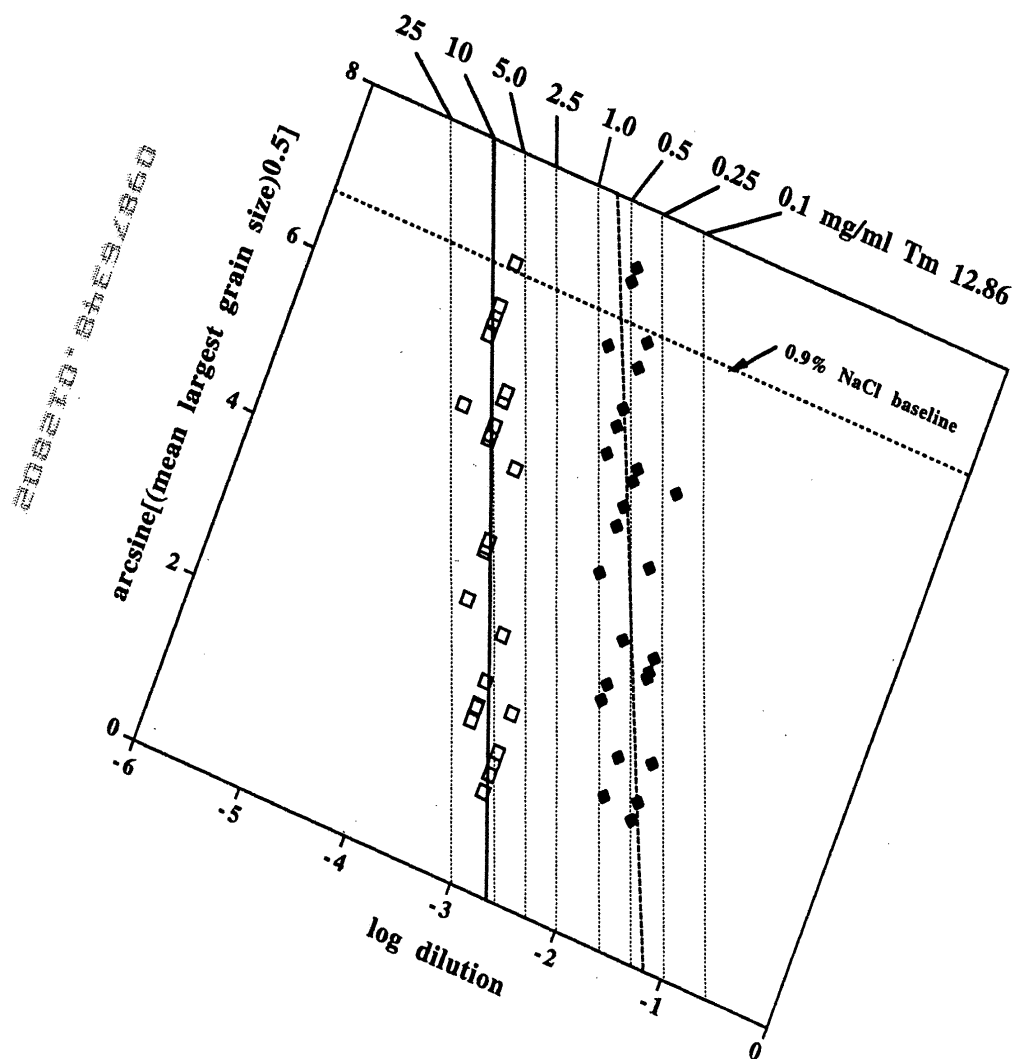


Fig. 8.26

200270 31254860

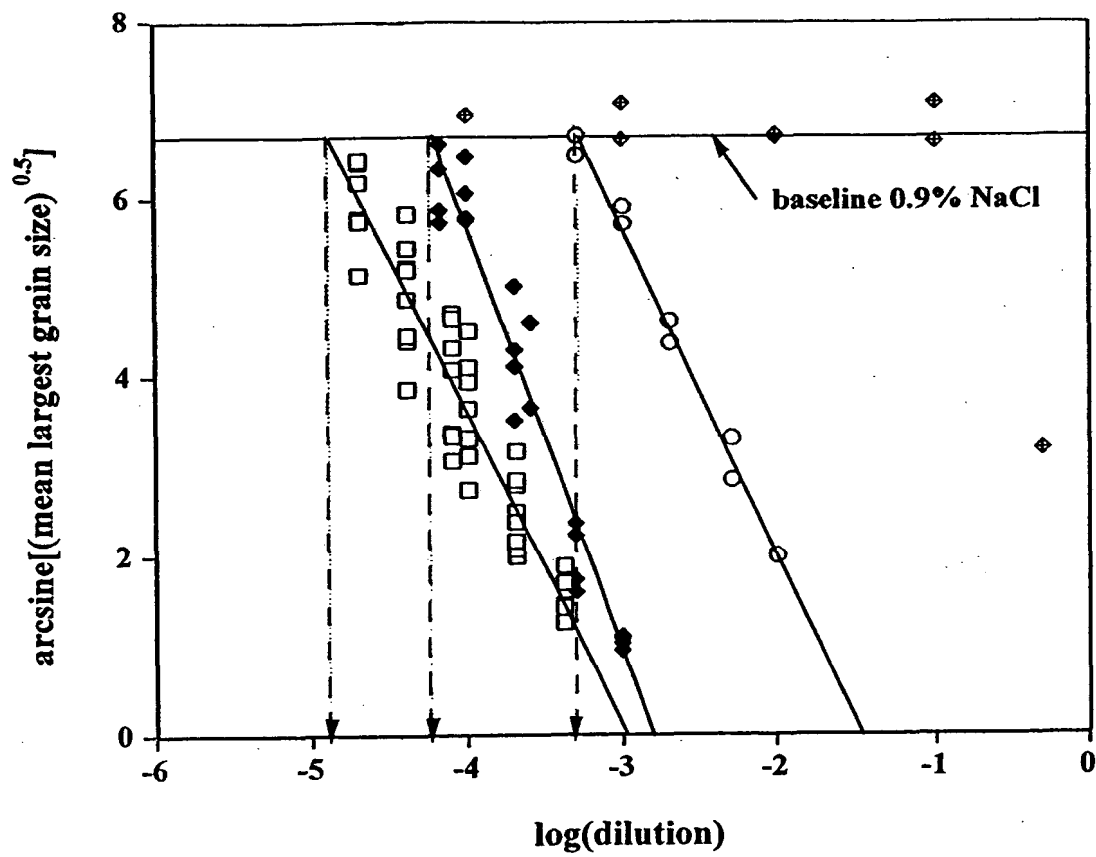


Fig. 8.27

2025-05-28 09:28:00

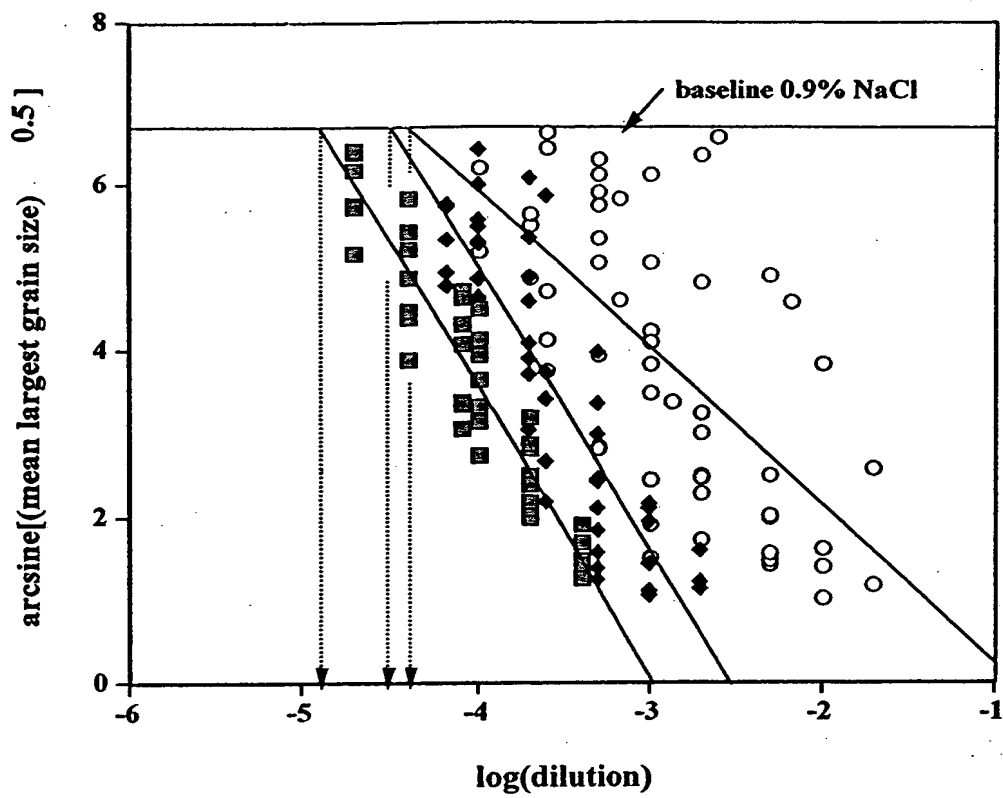


Fig. 8.28

202510-01E9.000

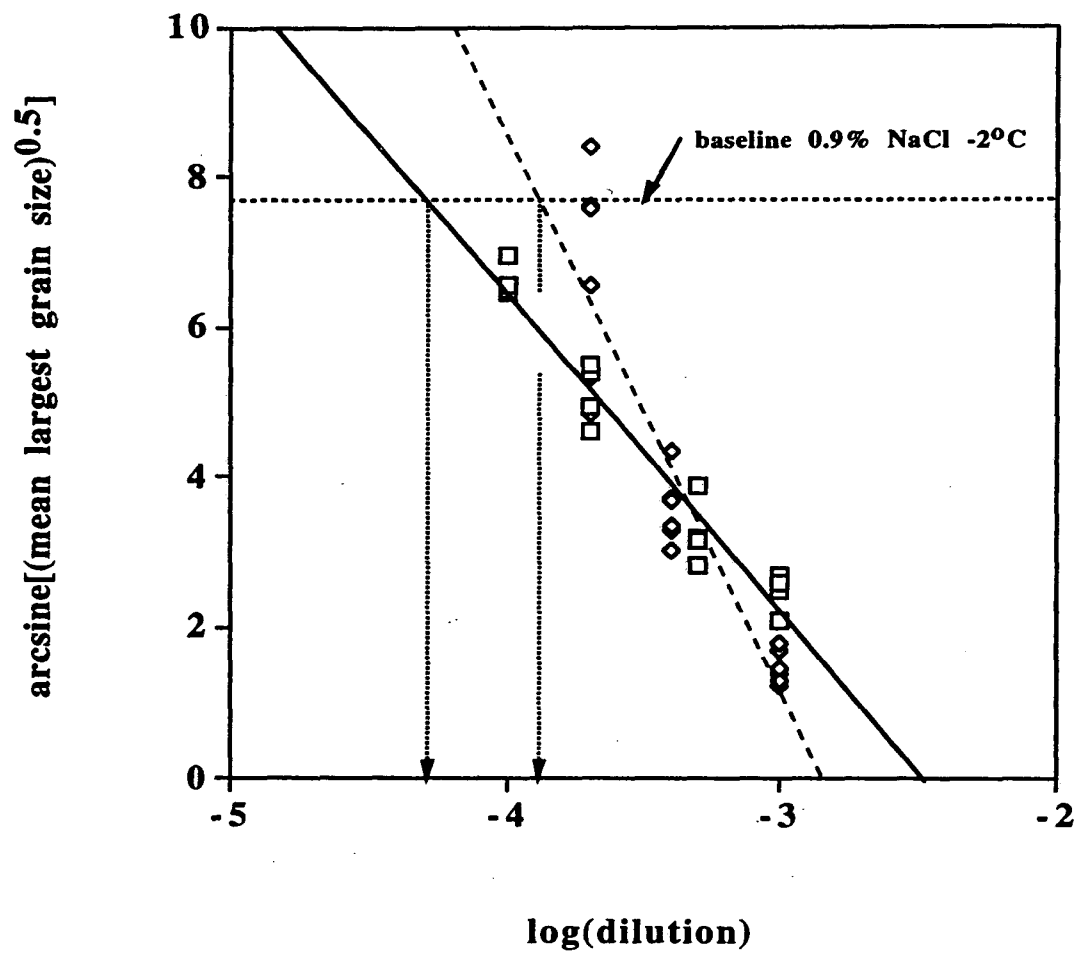


Fig. 8.29

202510 01194960

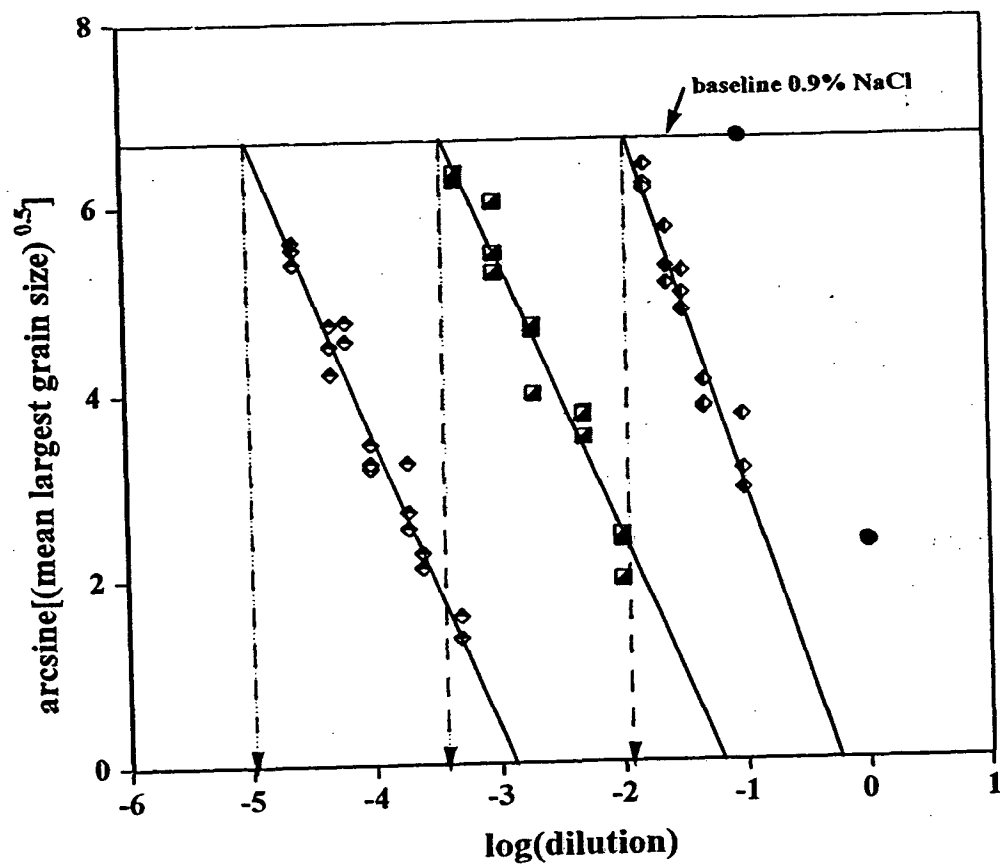


Fig. 8.30

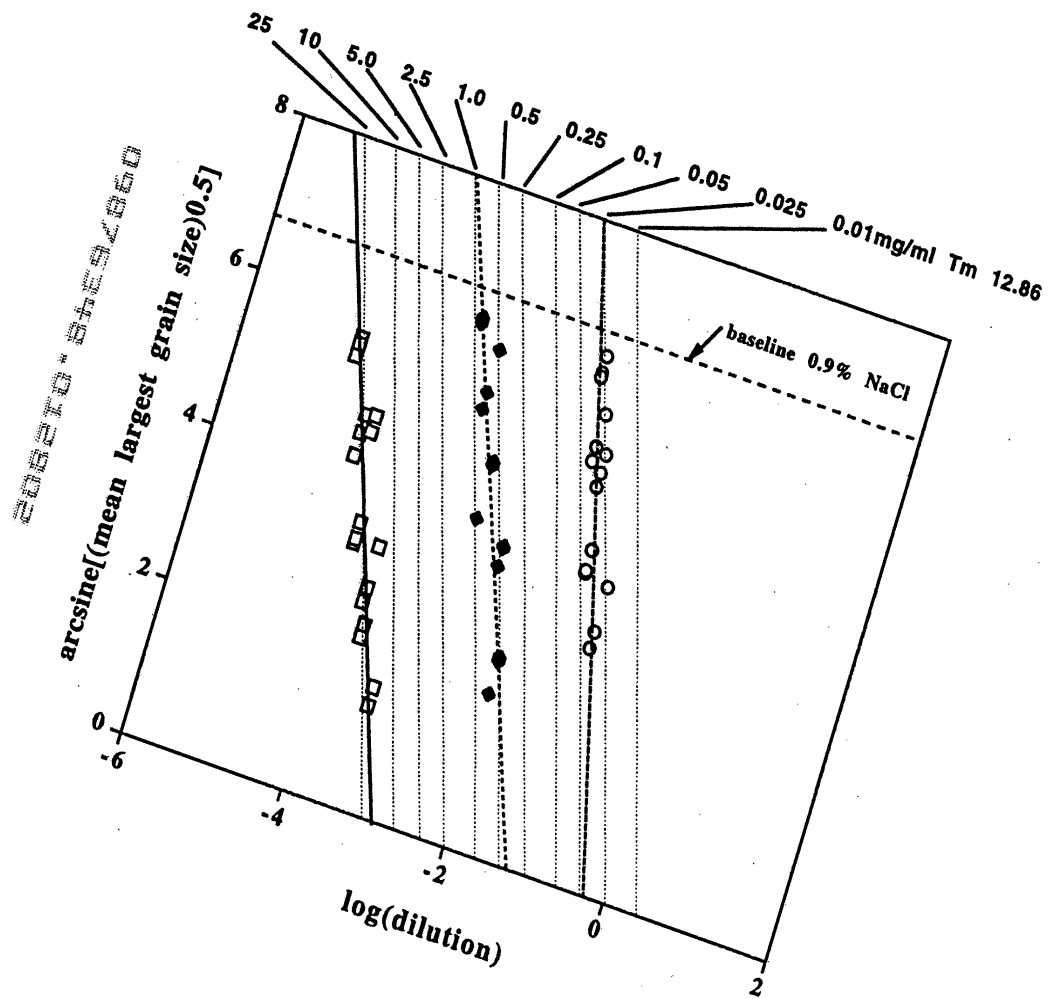


Fig. 8.31

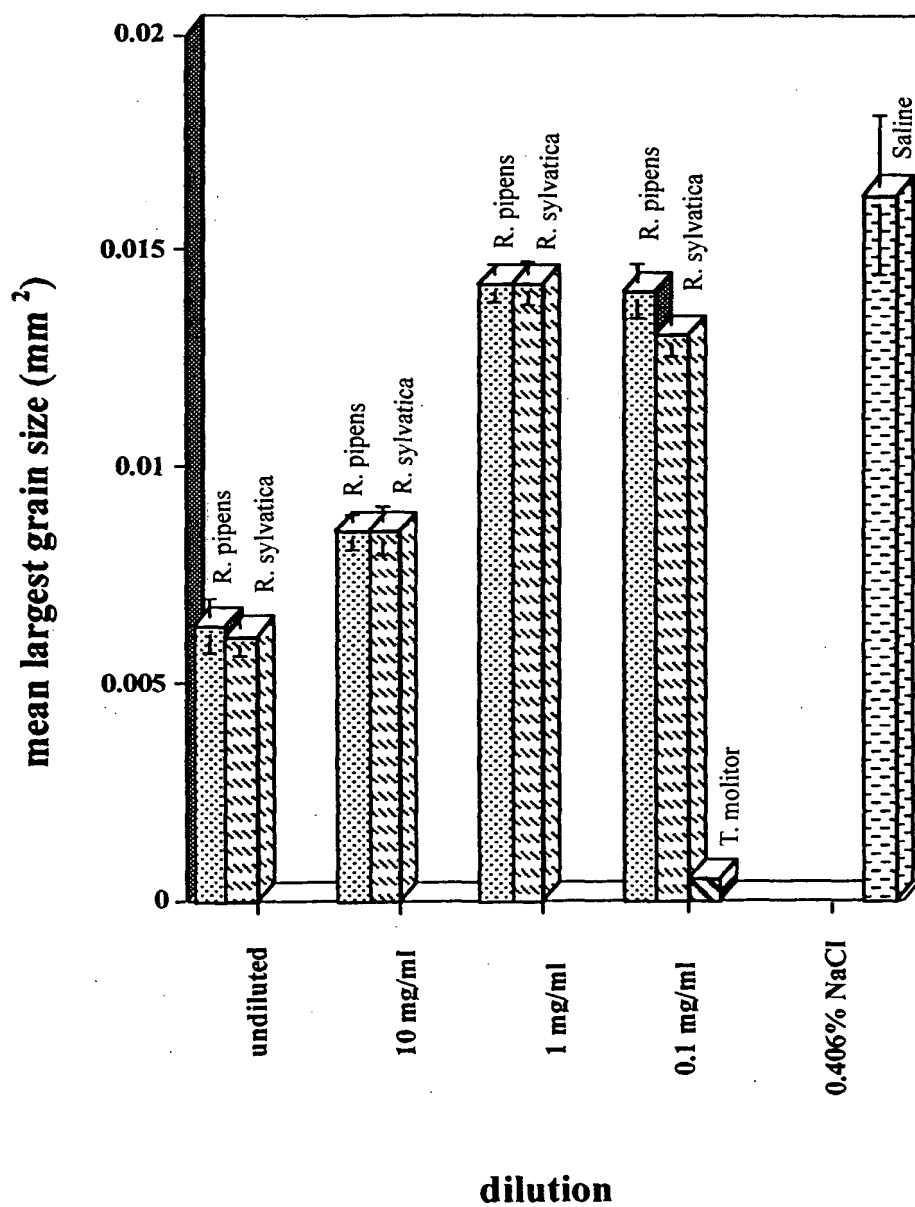


Fig. 8.32

205210 37E92860

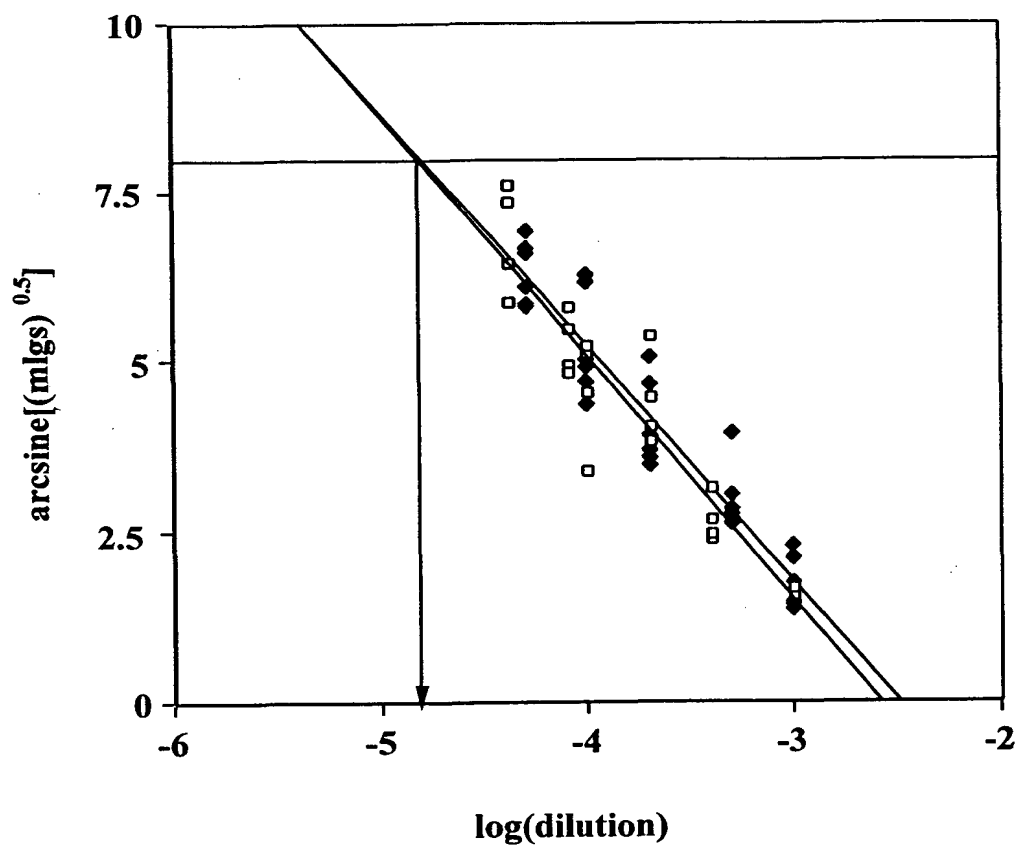


Fig. 8.33

202210 010 010 010

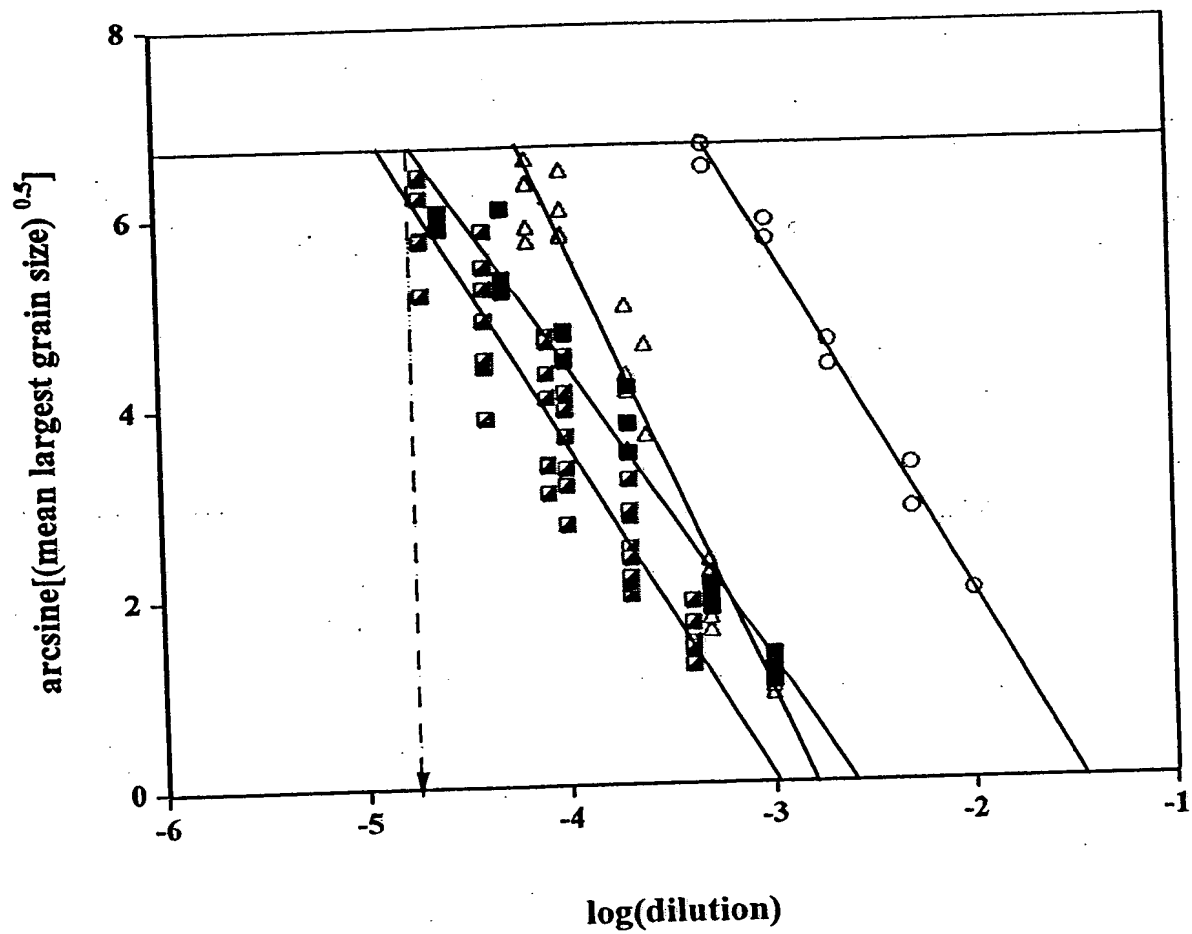


Fig. 8.34

00000 00000 00000

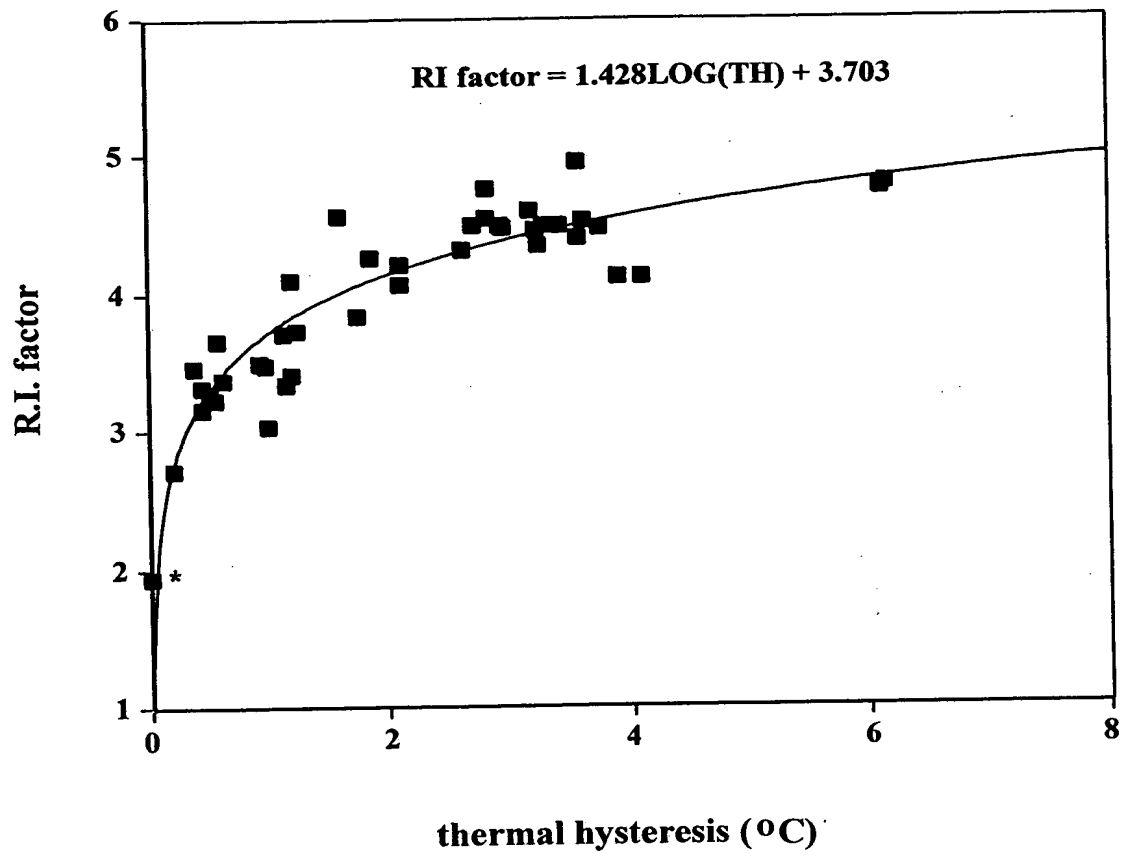


Fig. 8.35

202510-01E92B60

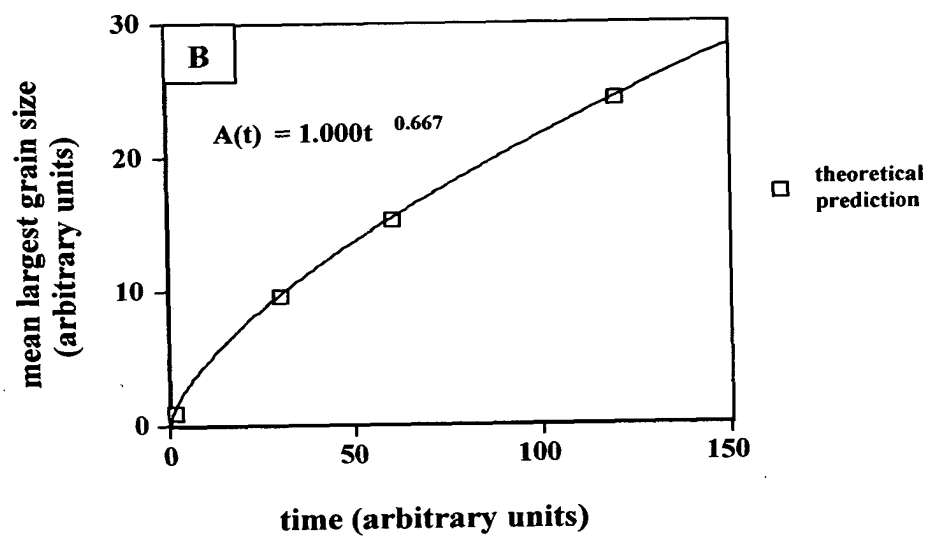
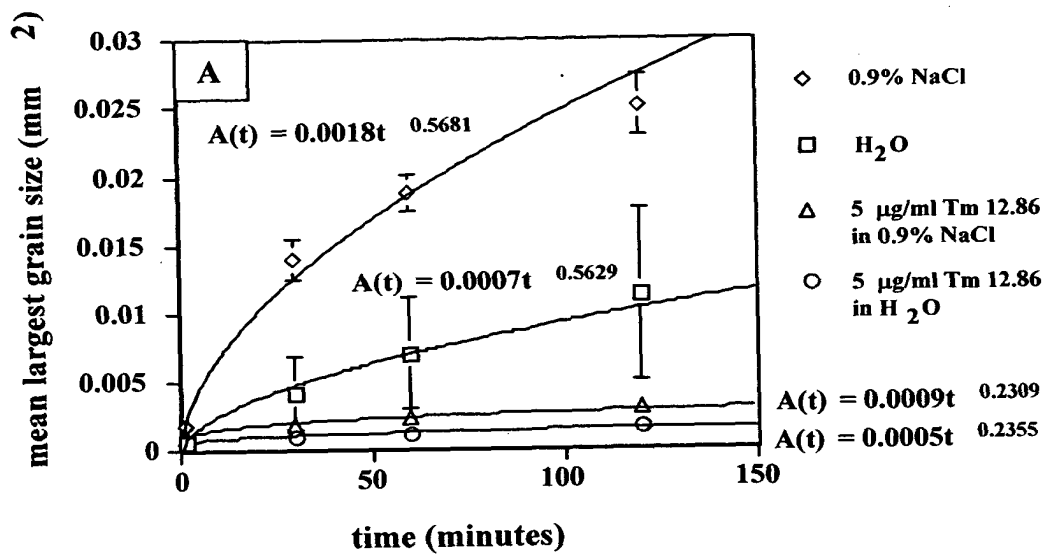


Fig. 8.36

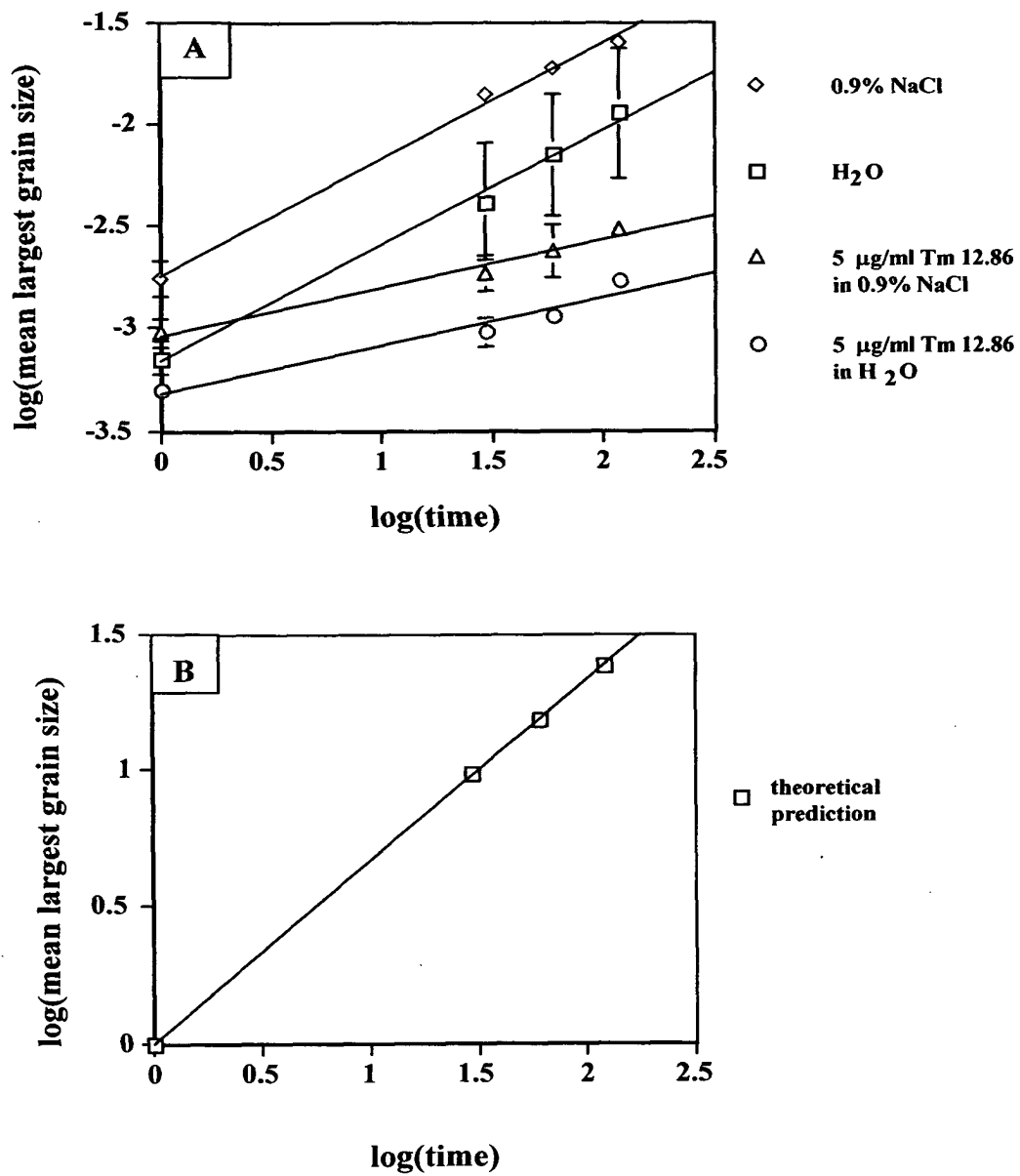
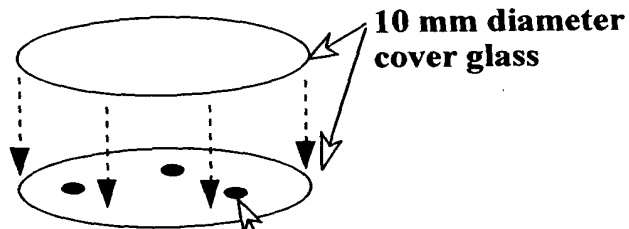


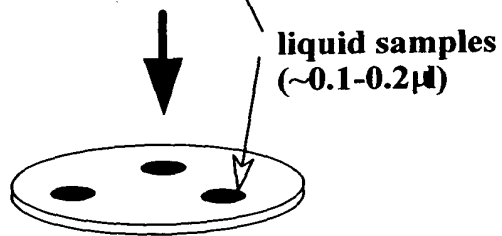
Fig. 8.37

"Sandwich" method of R.I. assessment

1.



2.



3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~ 10 MIN.)

4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS

Fig. 8.38

0907E349 042300

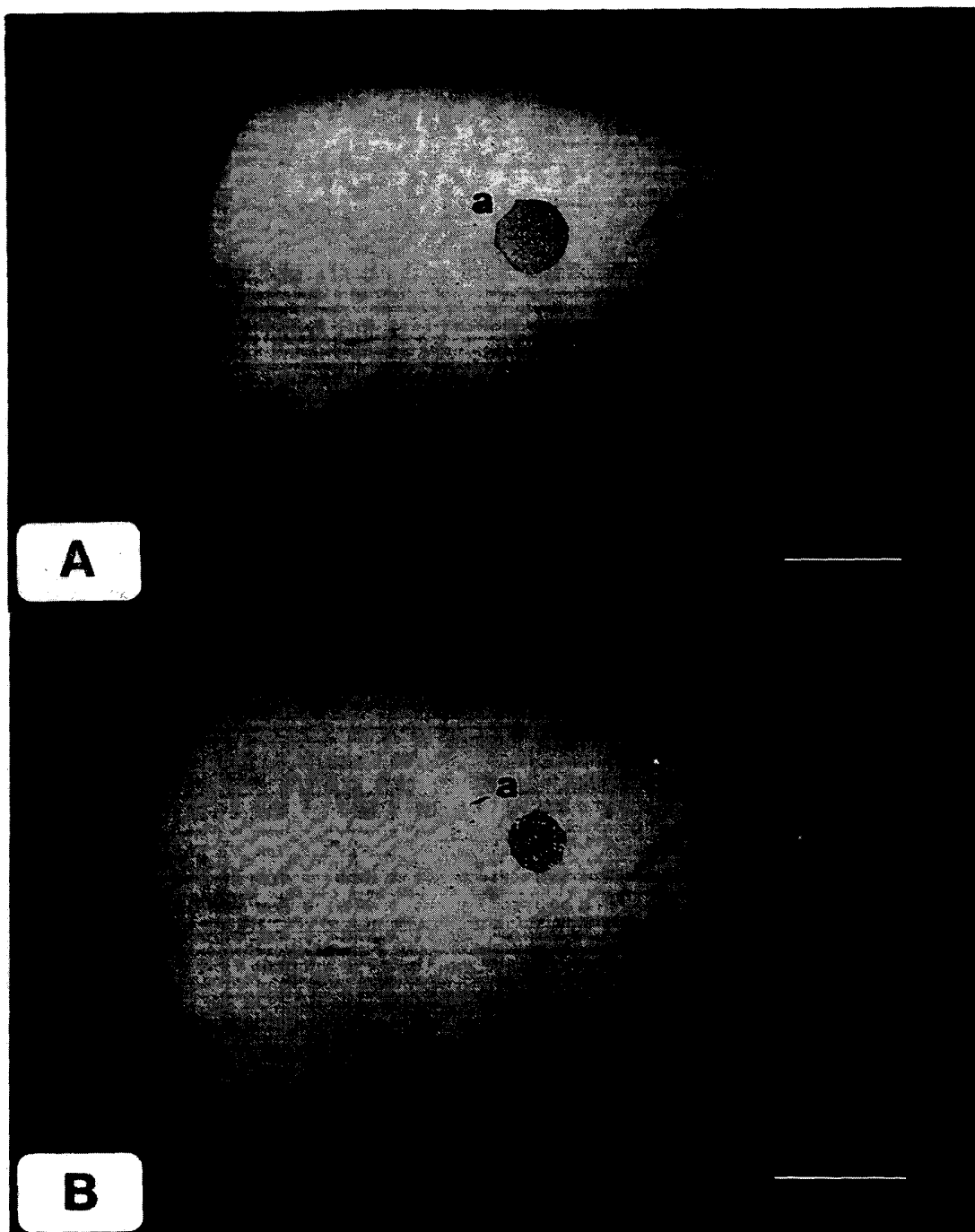


Fig. 8.39

20070 01252560

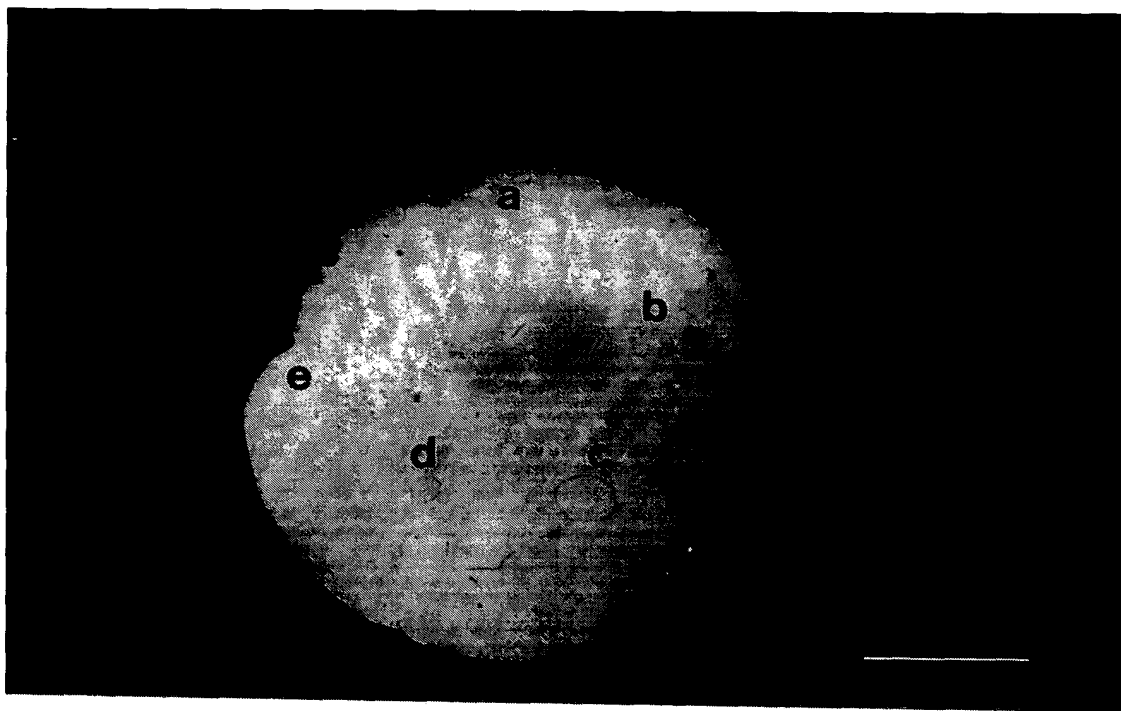


Fig. 8.40

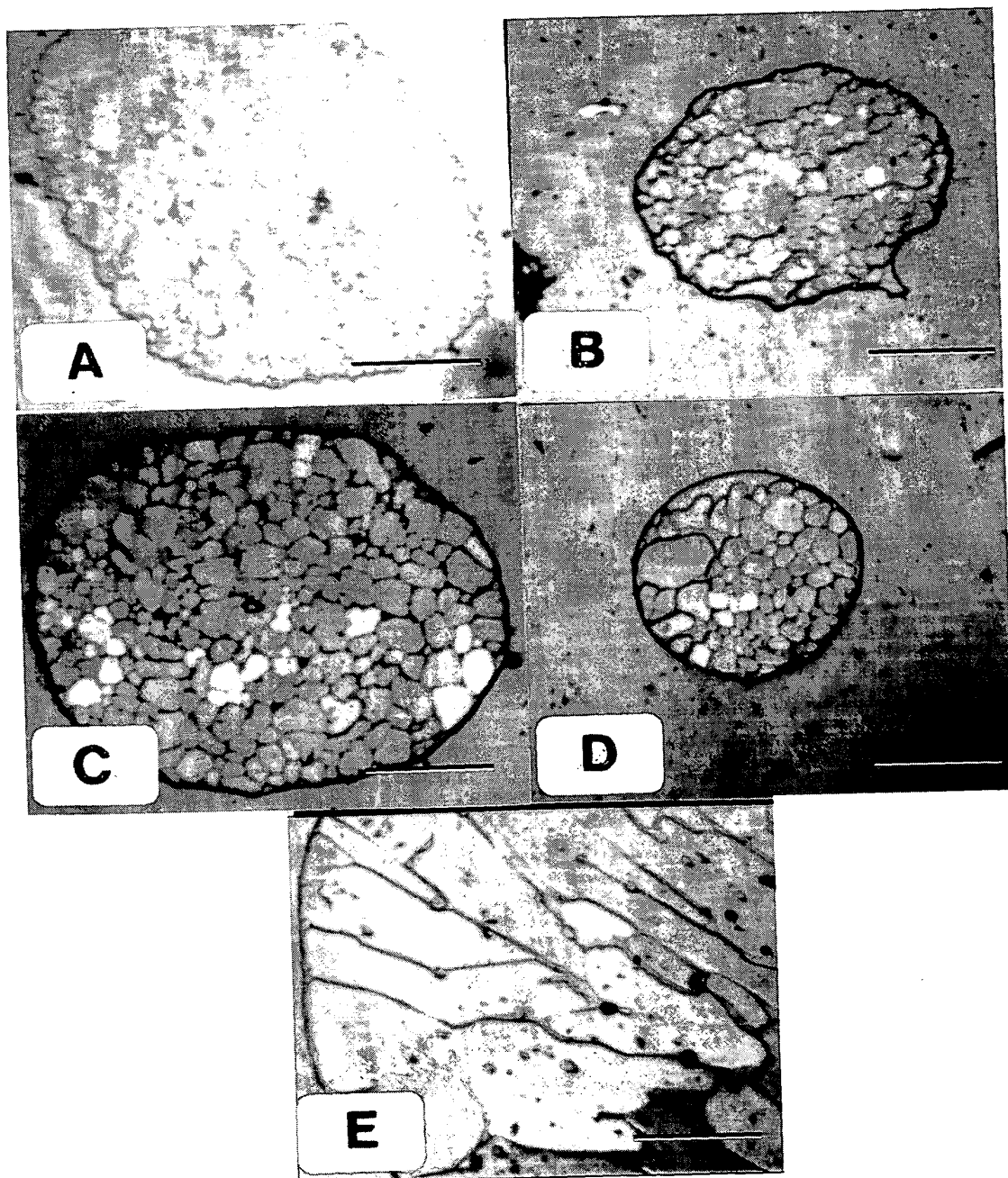


Fig. 8.41

095710 01E3/860

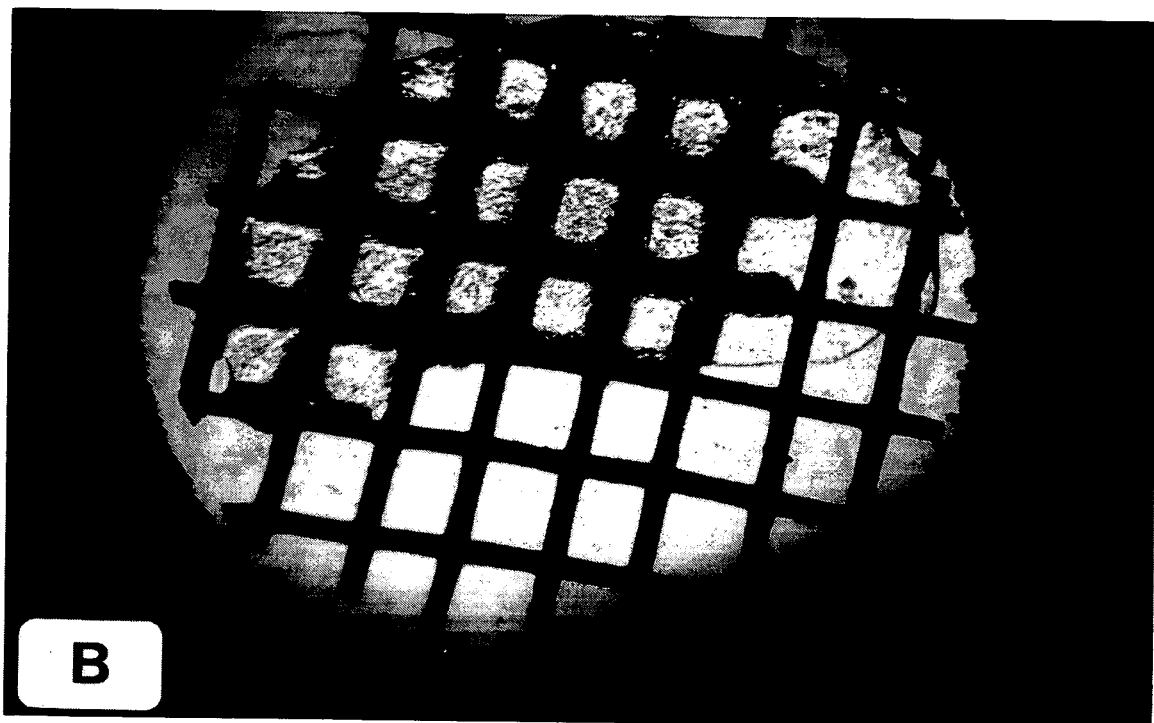
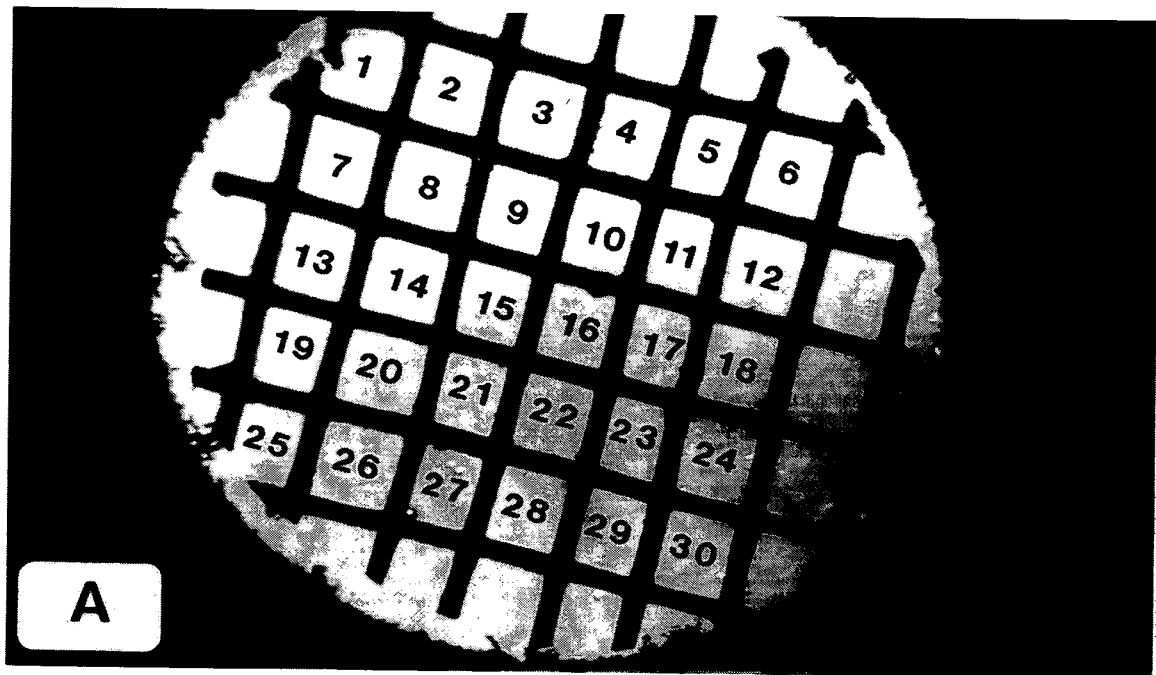


Fig. 8.42

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAANTTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTCTGCAAGAGATCATAACCAAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCCTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTCCGCCGTCAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

481 ATATAAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCATCGTTTCCACCC

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Fig. 8.43

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1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTCCGCCGCC
M K L L L C F A F A A P

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K P G

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S Y

137 CAAGAAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D Y

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y P

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P P G

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 8.44